

Dimensions of Biodiversity



National Science Foundation 2010 – 2012 Projects

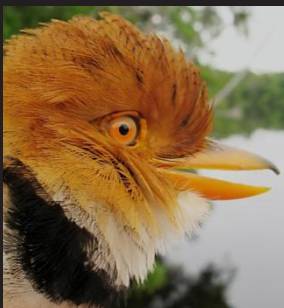


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Acknowledgements

Many NSF staff members, too numerous to mention individually, assisted in the development and implementation of the Dimensions of Biodiversity competitions that resulted in the projects described herein. The Dimensions of Biodiversity investigators are thanked and congratulated for their creativity and achievements in the research and coordination activities that these exciting projects represent. Finally, we are grateful to Dr. Sean M. Watts and Dr. Sara Chun, AAAS Science and Technology Policy Fellows, who were most helpful in strategic planning for Dimensions of Biodiversity, and the production of this abstract book.

Introduction

Earth is losing species more rapidly than scientists can understand the roles they play and how they function. With this species loss, humanity is forfeiting opportunities to understand the history of life, to better predict the future of the living world, and to make beneficial discoveries in the domains of food, fiber, fuel, pharmaceuticals, and bio-inspired innovation.

The National Science Foundation (NSF) is now in the fourth year of the 10-year Dimensions of Biodiversity program to characterize the least-well-known aspects of the diversity of life on Earth. NSF funded 14 new projects in FY 2012 bringing the total number of active projects to 41. Identifying species is just a first step in the journey of assessing the planet's biological diversity, but for many organisms even this step is far from complete. For example, insects are among the most diverse organisms and the total number of named, living insect species is estimated at 720,000. However, this represents as little as 7% of our 'best guesses' of insect diversity (4-10 million species)¹. Furthermore, all species rely on a vast network of mostly invisible and largely unknown life forms (bacteria, fungi, etc.), that far outnumber the more obvious organisms on the planet in both abundance and diversity. Beyond taxonomy, the genetic diversity within even a single species can be vast. The tremendous variation among domestic dog breeds illustrates this, and the genetic diversity within crop plants continues to play a critical role in agriculture. Finally, species and genetic diversity are best understood in a phylogenetic context that reflects the interaction networks, past and present, that have shaped the functional dimension, including but not limited to ecological, physiological, behavioral, cellular, and even molecular patterns and processes. Despite centuries of study, we still have much to learn about the origin and maintenance of diversity.

The innovative and interdisciplinary teams of the Dimensions of Biodiversity program “may accomplish in 10 years what, with a piecemeal approach, would have taken 50 years – a half-century we can no longer afford to wait.”

Dr. Joann P. Roskosi
NSF Deputy Assistant Director
for Biological Sciences

Addressing the substantial knowledge gaps in our understanding of biodiversity will require new thinking and a coordinated effort among several sub-disciplines of biology. An important distinction of the Dimensions initiative is the *simultaneous* investigation of the links and feedbacks between genetic, taxonomic/phylogenetic, and functional dimensions of biodiversity.

The Dimensions of Biodiversity program is actively developing the workforce and partnerships necessary for the unique human- and cyber-infrastructure challenges of an interdisciplinary network of researchers. Dimensions is partnering with NASA to fund

projects that use remote sensing technologies to expand biodiversity investigations across broad spatial and temporal scales.

International partnerships with the Chinese National Natural Science Foundation (NSFC) and two Brazilian funding agencies [Federal Agency for Support and Evaluation of Graduate Education of the Federative Republic of Brazil (CAPES) and the São Paulo Research Foundation (FAPESP)] will support the exchange of students and scientists, joint research projects, university partnerships and the digitization of biological collections.

Dimensions is also using a Distributed Graduate Seminar to baseline what is currently known about the genetic, taxonomic/phylogenetic, and functional dimensions of biodiversity. This baseline assessment will be posted on a wiki, crowd-sourced regularly by the broader scientific community, and “frozen” periodically to allow assessment of progress.

Improving how we describe the scope and role of life on Earth will require novel, interdisciplinary and coordinated approaches. In rising to this challenge, Dimensions of Biodiversity will redefine the way we understand the evolutionary and ecological significance of biodiversity in today’s changing environment, and in the geologic past.

“By establishing durable networks of interdisciplinary, globally-engaged scientists, the Dimensions of Biodiversity program will have a lasting positive effect on biodiversity science, with the potential to transform the way we conduct biological research in this area.”

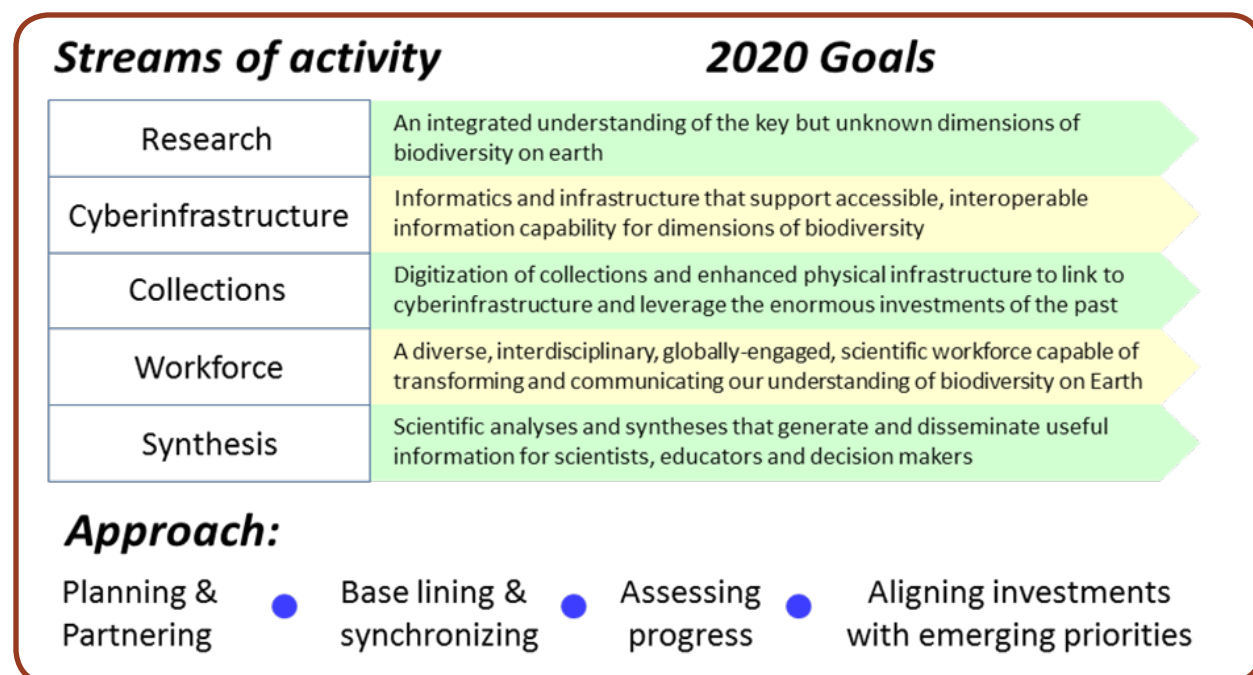
Dr. John C. Wingfield
NSF Assistant Director for
Biological Sciences

¹ Finlay, BJ, JA Thomas, GC McGavin, T Fenchel and RT Clarke. 2006. Self-similar patterns of nature: Insect diversity at local to global scales. *Proceedings of the Royal Society B*. 273: 1935-1941.



Dimensions of Biodiversity

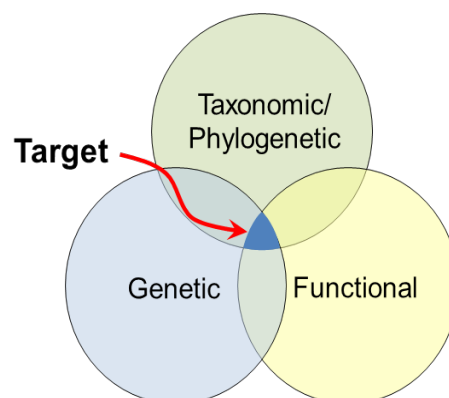
Dimensions of Biodiversity involves five streams of activity. The approach for supporting these activities involves planning and partnering, developing baselines of our current understanding, and assessing progress periodically during the decade in order to align investments with newly-appreciated priorities.



By 2020, Dimensions of Biodiversity is expected to have transformed our understanding of the scope and role of life on Earth and how biodiversity science is conducted. The initial focus of Dimensions has been on the integration of genetic, taxonomic/phylogenetic, and functional aspects of biodiversity (right). The goal of this activity, which complements core programs at NSF, is to *rapidly integrate the dimensions of biodiversity about which we know the least*.

The first of the annual competitions for research awards was held in 2010. In 2010 and 2011 a partnership with NSF-China supported International Research Coordination Network projects. In 2012 the partnership with NSF-China was expanded to include collaborative research projects, and a new partnership was established with the State of Sao Paulo, Brazil that also supports collaborative research projects. NASA also joined as a partner in 2012, to support research projects that use remote sensing.

- FY 2010: 16 projects (US Total ~\$25.7M: BIO \$18.9M; other NSF \$6.8M; NSF-China: ~\$108K)
- FY 2011: 11 projects (US Total ~\$28.0M: BIO \$17.5M; other NSF \$10.5M; NSF-China: ~\$93K)
- FY 2012: 14 projects (US Total ~\$26.4M: BIO \$21M; other NSF \$4.7M; NASA \$720K; NSF-China: \$2M; Brazil: \$2M)
- FY 2013 Partners: NASA (up to \$2M); funding agencies in China (up to \$5.2M) and Brazil (up to \$4M).



Fiscal Year 2012 Projects

US-China: An integrated understanding of how polyploidy generates biodiversity 10

Tia-Lynn Ashman, University of Pittsburgh (NSF 1241006); Aaron I. Liston, Oregon State University, Richard Cronn, U.S. Forest Service (NSF 1241217)

Species that are polyploidy contain more than two pairs of chromosomes. This project will examine the role that polyploidy has played in the evolution of a group of strawberry species growing in the US and in China.

Research on Airborne Ice Nucleating Species (RAINS) 12

Brent C. Christner, Louisiana State University (NSF 1241161); David C. Sands, Montana State University, Cindy Morris, INRA-PACA, (NSF 1241054); Boris A. Vinatzer, David Schmale, Virginia Tech (NSF 1241068); Carolyn F. Weber, Idaho State University (NSF 1241069)

This project will examine the diversity and activity of airborne microbes that catalyze the formation of ice crystals in the atmosphere. These ice nucleating organisms may influence cloud development, cloud chemistry, and ultimately weather.

US-BIOTA-Sao Paulo: Assembly and evolution of the Amazonian biota and its environment: An integrated approach 14

Joel L. Cracraft, American Museum of Natural History (NSF 1241066); Christopher W. Dick, University of Michigan (NSF 1240869); Robert P. Guralnick, University of Colorado (NSF 1241029); Kenneth E. Campbell, LA County Museum of Natural History (NSF 1241042); Andrew V. Brower, Middle Tennessee State University (NSF 1241056); John M. Bates, Field Museum of Natural History (NSF 1241075); Barbara M. Thiers, Scott Mori, New York Botanical Garden (NSF 1241127)

This project seeks to understand the evolutionary and ecological history of Amazonia, one of the most diverse ecosystems on Earth. A goal of the project is to build a comprehensive database of plants and vertebrates, which, together with remote sensing, geology, and Earth-systems modeling, will be used to understand how the Amazonian biota assembled across space and time.

Do parallel patterns arise from parallel processes? 16

Michael N. Dawson, John Berman, University of California Merced (NSF 1241255); Julian P. Sachs, University of Washington (NSF 1241247)

This project will examine the current and historical diversity in marine lakes that formed as melting ice sheets raised sea level. Many of these lakes were isolated from each other, providing opportunities for species in the lakes to evolve independently under similar environmental conditions.

The animal host as an engine of microbial diversity: Evolutionary pattern and ecological process shaping the gut microbiota of Drosophila species 18

Angela E. Douglas, Gregory Loeb, Cornell University; John Jaenike, University of Rochester (NSF 1241099)

This project will examine the microbial communities in the gut of fruitflies to understand how the fruit fly hosts and bacteria influence each other, and how this type of interaction may contribute to the process of evolution of hosts and the diverse assemblages of microbes that live within them.

Community assembly and decomposer function of aquatic fungi along a salinity gradient 20

Astrid Ferrer, James Dalling, Katy Heath, University of Illinois Urbana Champaign (NSF 1241212)

Diverse groups of freshwater and marine fungi remain to be described from tropical waters. This project will look at the role that these aquatic fungi play in the decomposition of wood along salinity gradients in coastal rivers in Panama.. A goal of the project will be to determine how gene expression patterns among these diverse fungi influence the rate and trajectory of wood decay in water.

A community level approach to understanding speciation in Hawaiian lineages 22

Rosemary G. Gillespie, John Harte, Rasmus Nielsen, Patrick O'Grady, University of California Berkeley (NSF 1241253); Daniel S. Gruner, University of Maryland (NSF 1240774); Kerry L. Shaw, Cornell University (NSF 1241060); Donald K. Price, University of Hawaii (NSF 1241228)

This project will examine arthropod communities on two Hawaiian islands to understand patterns and rates of evolution. The two islands differ in age, providing an opportunity to study evolution in multiple lineages in different ecological contexts.

The taxonomic, genomic, and functional diversity of soil carbon dynamics 24

Bruce A. Hungate, James Caporaso, Paul Dijkstra, Jane Marks, Egbert Schwartz, Northern Arizona University (NSF 1241094); Lance Price, Translational Genomics (NSF 1241115)

This project will examine the roles that taxonomic and genetic diversity of microbes play in the processing of new and old carbon in soils.

The role of taxonomic, functional, genetic, and landscape diversity in food web responses to a changing environment 26

Anthony R. Ives, Volker Radeloff, University of Wisconsin (NSF 1240804); Kerry M. Oliver, University of Georgia (1240892); Jason Harmon, North Dakota State University (NSF 1241031)

The project will examine how genetic, taxonomic, ecological, and landscape diversity influence the control of agricultural pests by their natural enemies.

The role of biodiversity for microbial adaptation to anthropogenic perturbations 28

Konstantinos T. Konstantinidis, Jim Spain, Eberhard Voit, Georgia Tech (NSF 1241046)

This project will examine how microbial species and communities respond to disturbance and to the presence of new organic compounds such as petroleum hydrocarbons, pesticides, and antibiotics.

Historical and contemporary influences on elevational distributions and biodiversity tested in tropical Asia 30

Thomas E. Martin, Robert Fleischer, Ellen Martinsen, University of Montana (NSF 1241041); Frederick H. Sheldon, Louisiana State University (NSF 1241059); Robert G. Moyle, University of Kansas (NSF 1241181)

This project will examine multiple factors that may contribute to the maintenance of elevational gradients in biodiversity, using a diverse tropical bird fauna in Borneo.

Anthropogenic nutrient input drives genetic, functional and taxonomic biodiversity in hypereutrophic Lake Taihu, China **32**

Hans W. Paerl, University of North Carolina (NSF 1240851); Wayne S. Gardner, University of Texas at Austin (NSF 1240798); Steven W. Wilhelm, University of Tennessee (NSF 1240870); Ferdinand L. Hellweger, Northeastern University (NSF 1240894)

This project will examine the species and genetic diversity of microbes in a lake that experiences massive blooms of toxic cyanobacteria, and link that diversity to the processing of nitrogen that is the cause of the toxic blooms.

US-China: Disentangling the components of tree biodiversity: Integrating phylogenies, functional traits and transcriptomes **34**

Nathan Swenson, Michigan State University (NSF 1241136)

This project will integrate genetic data with phylogenetic and functional trait approaches to the study of tree biodiversity, with the goal of developing a predictive framework that can be used to understand processes that generate and maintain forest diversity.

Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity **36**

Jonathan P. Zehr, Kbnigniew Kolber, University of California Santa Cruz (NSF 1241221); Kevin R. Arrigo, Stanford University (NSF 1241093); Matthew Church, University of Hawaii (NSF 1241263)

This project will use genomics, molecular biology, and stable isotope tracers to investigate how changes in the form and availability of nitrogen affect taxonomic, genetic, and functional diversity of marine phytoplankton.

Fiscal Year 2011 Projects

Diversity and symbiosis: Examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota

38

Lisa K. Belden, Leanna L. House, and Roderick Jensen, Virginia Polytechnic Institute and State University (NSF 1136640); Reid N. Harris, James Madison University (NSF 1136602); Kevin P. Minbiole, Villanova University (NSF 1136662)

This project will investigate the diverse microbial communities on the skin of amphibian species and their role in controlling a critical disease that threatens amphibian biodiversity in the Neotropics.

Integrating genetic, taxonomic, and functional diversity of tetrapods across the Americas and through extinction risk

40

Thomas Brooks, Gabriel C. Costa, and Bruce Young, NatureServe (NSF 1136586); Catherine Graham, State University of New York, Stony Brook (NSF 1136705); Stephen B. Hedges, Pennsylvania State University, University Park (NSF 1136590); Volker C. Radeloff, University of Wisconsin, Madison (NSF 1136592)

Brooks and colleagues will use a database of the 13,000 land vertebrates of the Americas to consider how changes in one dimension of biodiversity influences changes in others. Understanding how species composition influences the diversity of functional traits, for example, will improve the efficiency and effectiveness of conservation actions.

Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts

42

Jed A. Fuhrman, David A. Caron, John F. Heidelberg, William C. Nelson, and Fengzhu Sun, University of Southern California (NSF 1136818)

Fuhrman and colleagues will compare heavily disturbed harbor regions and relatively pristine ocean habitat in the Los Angeles basin to better understand links between marine microbial diversity and ecosystem function.

Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, *Inga*

44

Thomas Kursar and Phyllis D. Coley, University of Utah (NSF 1135733)

*This project will study interactions between members of the tree genus *Inga* (>300 species) and their insect herbivores at five sites in Central and South America. This work will shed light on the coevolution of plants and herbivores and its influence on the ecology of the most diverse forest communities on Earth.*

Lake Baikal responses to global change: The role of genetic, functional and taxonomic diversity in the plankton

46

Elena G. Litchman and Christopher A. Klausmeier, Michigan State University (NSF 1136710); Stephanie E. Hampton, University of California, Santa Barbara (NSF 1136637); Marianne Moore, Wellesley College (NSF 1136657); Edward C. Theriot, University of Texas, Austin (NSF 1136667); Lev Yampolsky, East Tennessee State University (NSF 1136706)

This project will study the planktonic food web of the world's largest, oldest, and most biologically diverse lake - Lake Baikal in Siberia -to predict how native vs. non-native plankton will respond to accelerating environmental change in this system.

Integrating dimensions of Solanum biodiversity: Leveraging comparative and experimental transcriptomics to understand functional responses to environmental change

48

Leonie C. Moyle, David C. Haak, and Matthew W. Hahn, Indiana University (NSF 1136707)

This research will highlight the role of drought and herbivore defense in driving the remarkable diversity of wild tomato species. Given the economic importance of tomatoes and their relatives (e.g. peppers, potatoes), studies of this sort will help prepare societies for the future challenges facing global food security.

Functional diversity of microbial trophic guilds defined using stable isotope ratios of proteins

50

Ann Pearson and Peter Girguis, Harvard University (NSF 1136484); Jennifer Macalady, Pennsylvania State University, University Park (NSF 1136218)

This project will use isotopic ratios of carbon, nitrogen, hydrogen, and sulfur produced during microbial metabolism to link guilds of microbes to their roles in biogeochemical and ecosystem processes. This novel approach will contribute to our understanding of what maintains functional and genetic diversity in microbes and, by extension, the roles those microbes play in ecosystems.

The climate cascade: Functional and evolutionary consequences of climatic change on species, trait, and genetic diversity in a temperate ant community

52

Nathan J. Sanders, University of Tennessee, Knoxville (NSF 1136703); Robert P. Dunn, North Carolina State University (NSF 1136717); Aaron M. Ellison, Harvard University (NSF 1136646); Nicholas J. Gotelli, Bryan A. Ballif, and Sara I. Cahan, University of Vermont and State Agricultural College (NSF 1136644)

Sanders and colleagues will study adaptations to climate change in a common foraging ant in eastern US forests to understand the mechanisms that allow some species to adapt to shifts in climate rather than migrating or going extinct.

An integrated study of energy metabolism, carbon fixation, and colonization mechanisms in chemosynthetic microbial communities at deep-sea vents

54

Stefan M. Sievert, Jeffrey S. Seewald, and Craig D. Taylor, Woods Hole Oceanographic Institution (NSF 1136727); Dionysios I. Foustoukos, Carnegie Institution of Washington (NSF 1136608); Ramunas Stepanauskas, Bigelow Laboratory for Ocean Sciences (NSF 1136488); Costantino Vetriani, Rutgers University, New Brunswick (NSF 1136451)

This project will establish an interdisciplinary, international research program to better understand the underlying microbiology and biogeochemistry in deep-sea hydrothermal vent ecosystems.

Functional diversity of marine eukaryotic phytoplankton and their contributions to C and N cycling

56

Bess B. Ward and Daniel M. Sigman, Princeton University (NSF 1136345); Andrew E. Allen, J. Craig Venter Institute, Inc. (NSF 1136477)

This project will use two North Atlantic sites in two seasons to link genetic diversity and species composition of phytoplankton communities to the biogeochemistry of the surface ocean.

INTERNATIONAL RESEARCH COORDINATION NETWORK: A research coordination network for biodiversity of ciliates

58

PI: John Clamp, North Carolina Central University (NSF 1136580)

Steering Committee:

US MEMBERS: John Clamp; Laura Katz, Smith College; Chris Lobban, University of Guam; Micah Dunthorn, University of Kaiserslautern, Germany

CHINA MEMBERS: Weibo Song, Ocean University of China, Qingdao; Xiaofeng Lin, South China Normal University, Guangzhou.

OTHER COUNTRIES: Alan Warren, Natural History Museum, London, United Kingdom; Laura Utz, Pontifícia Universidade Católica do Rio Grande do Sul, Brazil

This project, jointly supported by the National Natural Science Foundation of China, will establish an International Research Coordination Network for Biodiversity of Ciliates. The network will include researchers from the US, China, the UK, and Brazil and will broaden exploration of these important protists.

Fiscal Year 2010 Projects

The microbial basis of animal speciation

60

Seth Bordenstein, Vanderbilt University (NSF 1046149)

This project will investigate the role host-associated microbial communities play in structuring species complexes and diversification in a genus of parasitoid wasps.

Deconstructing diversity and ecosystem function at multiple spatial and genetic scales in a keystone plant-microbe symbiosis

62

Thomas Bruns and John W. Taylor, University of California, Berkeley (NSF 1046115); Kabir G. Peay, University of Minnesota – Twin Cities (NSF 1045658); Rytas Vilgalys, Duke University (NSF 1046052)

This project will consider soil fungal communities associated with pine-dominated forests in North America, which are poorly known and may serve as a model system for understanding microbial community dynamics.

Can evolutionary history predict how changes in biodiversity impact the productivity of ecosystems?

64

Bradley Cardinale, University of Michigan Ann Arbor (NSF 1046121); Charles F. Delwiche, University of Maryland College Park (NSF 1046075); Todd H. Oakley, University of California Santa Barbara (NSF 1046307)

Cardinale and colleagues will examine how evolutionary processes among algae generate and maintain diversity at levels from genes to ecosystems in freshwater lakes.

Functional, genetic, and taxonomic diversity of plant-fungal interactions along climatic gradients and their role in climate change driven species migrations

66

Richard Lankau, University of Georgia (NSF 1045977)

The largely unseen world of soil fungi is intimately linked to plant communities. This award supports research to understand how the taxonomic diversity of soil fungi interacts with the genetic diversity of two tree species.

Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host

68

Carol Lee, University of Wisconsin Madison (NSF 1046372); Joana Carneiro da Silva, University of Maryland, Baltimore (NSF 1046371)

This project characterizes diversity and metabolic functions of the microbiome of a copepod, and will test how the diversity and functions (metabolic and ecological) change when the saline copepod invades a novel habitat (fresh water).

- An interdisciplinary study of hyperdiverse endophytic fungi and their function in boreal forests*** 70
 Francois Lutzoni, Duke University (NSF 1046065); Anne Arnold, University of Arizona (NSF 1045766); Ignazio Carbone, North Carolina State University (NSF 1046167); Georgiana May, University of Minnesota, Twin Cities (NSF 1045608)
This project investigates a diverse and poorly described group of endophytic fungi with symbiotic relationships to boreal vascular plants and lichens.
- Biological controls in the ocean: the Redfield Ratio*** 72
 Adam Martiny and Steven Allison, University of California Irvine (NSF 1046297); Simon Levin, Princeton University (NSF 1046001); Michael Lomas and Benjamin Van Mooy, Bermuda Institute of Ocean Sciences (NSF 1045966); and Kun Zhang, University of California San Diego (NSF 1046368)
The Redfield ratio is the ratio of nitrogen to phosphorus in seawater. Understanding how biodiversity regulates the Redfield ratio will provide important insights for understanding the role of biodiversity in regulating global nutrient cycles.
- Genomics, functional roles, and diversity of the symbiotic gut microbiotae of honey bees and bumble bees*** 74
 Nancy Moran, Yale University; and Jay Evans, USDA ARS (NSF 1046153)
Most of Earth's biodiversity is microbial. This project will examine the microbiota in the guts of bees from two genera – Apis (honey bees) and Bombus (bumblebees). The research will offer important insights into the ecological resilience of organisms that provide economic, ecological, and agricultural value through their pollination services.
- An integrative traits-based approach to predicting variation in vulnerability of tropical and temperate stream biodiversity*** 76
 N. Leroy Poff, William C. Funk, Cameron Ghalambor, and Boris Kondratieff, Colorado State University (NSF 1046408); Alexander Flecker, Joseph Bernardo, and Kelly Zamudio, Cornell University (NSF 1045960); and Steven Thomas, University of Nebraska Lincoln (NSF 1045991)
Predicting the effects of rapid climate change on biodiversity is an important and urgent scientific challenge. This project will examine the influence of climate change on stream biodiversity in a tropical stream system in the Andes of Ecuador and a temperate alpine stream system in the Colorado Rockies.
- Shedding light on viral dark matter—genetic, taxonomic, and functional diversity of coral reef viromes*** 78
 Forest Rohwer, Robert A. Edwards, and Anca Segall, San Diego State University (NSF 1046413)
This project will examine virus diversity on coral reefs along a gradient of human-caused effects at both regional and global scales.
- Parallel evolutionary radiations in Protea and Pelargonium in the Greater Cape Floristic Region*** 80
 Carl Schlichting, Kent Holsinger, Cynthia Jones, and John Silander, University of Connecticut (NSF 1046328); Andrew Latimer, University of California Davis (NSF 1045985); Justin Borevitz, University of Chicago (NSF 1046251)
The fynbos and succulent karoo biomes in South Africa's Greater Cape Floristic Region are two of the world's plant biodiversity hotspots. Using these two plant genera as model systems, this project will look at the ways in which functional diversity of traits evolves and influences community dynamics.

Significance of nitrification in shaping planktonic biodiversity in the ocean 82

David Stahl, E. Virginia Armbrust, Allan Devol, and Anitra Ingalls, University of Washington (NSF 1046017)

Stahl and others will examine the diversity and function of ammonia oxidizing Archaea (AOA) in the ocean and determine the role of these newly discovered organisms in structuring the diversity of phytoplankton.

The role of viruses in structuring biodiversity in methanotrophic marine ecosystems 84

David Valentine, University of California, Santa Barbara (NSF 1046144)

Microbes in ocean sediments form a unique ecosystem. There methane is consumed, preventing large amounts of this potent greenhouse gas from entering the atmosphere. The research will shed light on a dark corner of the biosphere, and could identify new and novel genes that support life in these environments.

Roles of functional, phylogenetic, and genetic diversity in structuring and sustaining plant communities through environmental change 86

Donald Waller, Kenneth Cameron, Thomas Givnish, and Kenneth Sytsma, University of Wisconsin-Madison (NSF 1046355)

Waller and colleagues are examining the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants in Wisconsin forests and grasslands. Their goal is to identify how climate change, habitat fragmentation, invasive species, and overabundant deer are acting to drive ecological change.

Dimensions of Biodiversity Distributed Graduate Seminar 88

Julia Parrish, University of Washington (NSF 1050680)

A distributed graduate seminar will provide a baseline for the planned 10-year program. A synthesis of current understanding of the dimensions of biodiversity will be posted on a wiki, crowd-sourced regularly, and “frozen” periodically to allow assessment of progress.

INTERNATIONAL RESEARCH COORDINATION NETWORK: Diversity and forest change: Characterizing functional, phylogenetic and genetic contributions to diversity gradients and dynamics in tree communities 90

US TEAM: Stuart Davies, Harvard University; Nathan G. Swenson, Michigan State University; W. John Kress, Smithsonian National Museum of Natural History; Rick Condit, Center for Tropical Forest Science, Smithsonian Tropical Research Institute (STRI); and Helene Muller-Landau, STRI (NSF 1046113)

CHINA TEAM: Zhanqing Hao, Institute of Applied Ecology, Chinese Academy of Sciences (CAS); Keping Ma, Institute of Botany, CAS; Wanhui Ye, South China Botanical Garden, CAS; Jie Li, Xishuangbanna Tropical Botanical Garden, CAS; Xiangcheng Mi, Institute of Botany, CAS; Xugao Wang, Institute of Applied Ecology, CAS.

This project is the first to be funded by the partnership between NSF and the National Natural Science Foundation of China. A group of forest scientists from the US, China, and other parts of Asia has created an international research coordination network (IRCN) to explore the resilience of forests to global change.

US-China: An integrated understanding of how polyploidy generates biodiversity

Tia-Lynn Ashman, University of Pittsburgh (NSF 1241006); Aaron I. Liston, Oregon State University, Richard Cronn, U.S. Forest Service (NSF 1241217))

Species that are polyploid contain more than two pairs of chromosomes. This project will examine the role that polyploidy has played in the evolution of a group of strawberry species growing in the US and in China.

All flowering plants possess two or more copies of every chromosome. Polyploidy is thought to be a main driver of plant speciation, biological adaptation and range expansion. How chromosome doubling contributes to biodiversity, and which genomic mechanisms or functional traits underlie the success of polyploids, remain unanswered questions.

This project will focus on wild species of strawberry (genus *Fragaria*). Nearly half of the 20 species of wild strawberry are polyploid and the genus has centers of diversity in China and North America. Strawberries possess numerous features (small genome, clonal propagation, availability of synthetic neopolyploids, sensitivity to climate change due to early-spring flowering and northern latitude or high elevation distribution) that make them an outstanding model system to better understand how genome doubling contributes to biodiversity. Research will focus on seven ‘trios’ of polyploid species and their diploid progenitors, native to North America, Europe and East Asia. Extensive field work will be conducted in China, focused on East Asian species that are poorly known ecologically and taxonomically.

This research will establish whether similarities in functional diversity and ecological amplitude of polyploid species are the result of common rules of genetic diversity, chromosome structure or gene expression in a polyploid genome, or whether multiple genetic and genomic pathways lead to

successful responses to environmental change. Deep phylogenetic and population genomic sampling will determine whether multiple independent origins contribute to functional and genetic diversity of natural polyploids. The characterization of trait and gene expression in natural and synthetic polyploids, and their diploid progenitors, under climatically diverse experimental gardens (eastern USA, western USA, China) will identify how functional and genetic diversity are distributed in a polyploid/diploid lineage. The integration of these results will inform efforts to predict the effect of whole genome duplication on ecological and evolutionary responses to environmental change in numerous other plant lineages.

This project will accelerate our understanding of how genome doubling confers success, and how it contributes to biodiversity across geographic and evolutionary scales. Moreover, this deeply integrated comparative study of the wild relatives of the cultivated strawberry – a polyploid species of world-wide economic importance – will provide foundational knowledge and contribute unparalleled resources that may be harnessed in efforts to ensure sustainability of strawberry and related crops (e.g., cherry, peach, pear, apple) in the face of abiotic stress. The work will promote training by broad participation and international collaboration, and novel hands-on science curriculum for middle school and undergraduate students.



Above: Eagle Glacier and River, Juneau Alaska, a high latitude site of *Fragaria chiloensis*. [Arlo Midgett]



Above: *Fragaria chiloensis* fruit at Honeyman State Park, Florence, Oregon. [Tia-Lynn Ashman]



Strawberry polyploidy project collaborators at the H.J. Andrews Experimental Forest. Jacob Tennesen, Rich Cronn, Aaron Liston, Tia-Lynn Ashman, Chris Edwards. [Aaron Liston, Oregon State University]

Research on Airborne Ice Nucleating Species (RAINS)

Brent C. Christner, Louisiana State University (NSF 1241161); David C. Sands, Montana State University, Cindy Morris, INRA-PACA, (NSF 1241054); Boris A. Vinatzer, David Schmale, Virginia Tech (NSF 1241068); Carolyn F. Weber, Idaho State University (NSF 1241069)

This project will examine the diversity and activity of airborne microbes that catalyze the formation of ice crystals in the atmosphere. These ice nucleating organisms may influence cloud development, cloud chemistry, and ultimately weather.

Microorganisms are abundant in the atmosphere and widely distributed by air currents, yet little is known about the abundance, diversity, and flux of microorganisms in the atmosphere. Numerous studies have provided evidence that microorganisms in the atmosphere may affect cloud development, cloud chemistry, and thus weather patterns. Ice formation in clouds is important in the processes leading to precipitation, but at temperatures warmer than -36°C (-33°F), water drops in clouds require particles, ice nucleators, to initiate freezing. The most active naturally occurring ice nucleators are microorganisms with the capacity to catalyze freezing at temperatures near -2°C (28°F). This is accomplished by a specialized protein that serves as an 'ice template', aligning water molecules in a fashion that promotes freezing.

RAINS is motivated by the potential of ice nucleating microorganisms to significantly impact meteorology and use atmospheric precipitation as a dispersal strategy. Goals of this study are to: (1) characterize the taxonomic diversity in the lower atmosphere and precipitation (including precipitation that occurred between 1794 AD and present and which is preserved in glacial ice), (2) determine the genetic diversity of microbial assemblages and individual ice nucleating bacteria in the lower atmosphere, and (3) examine the role of precipitation and biological ice nucleation in disseminating microbes via the atmosphere.

RAINS will be transformative in determining which microbial taxa are carried to the Earth's surface via precipitation, which of these microbes are ice nucleators and may contribute to inducing precipitation, and which of these taxa present possible inoculum sources for diseases that impact humans, domestic animals, and plants.

RAINS will increase knowledge on the biodiversity and nature of the most active ice nucleators in the planetary boundary layer of the atmosphere, where important meteorological phenomena occur. Ice nucleation may allow certain microorganisms and plant pathogens to efficiently 'cycle' between the atmosphere and surface habitats, and RAINS will contribute to ongoing efforts to assess the movement of ice nucleating microorganisms at the geographical scale. Outreach efforts will take these advances into high school and college classrooms in the form of hands-on research experiences for students at both levels and will serve as the basis for high school educators to develop unique classroom activities. In addition, an international network of scientists collecting field data on the relationship between biological ice nucleator abundance, cropping patterns and precipitation in dry land regions will be established. RAINS will sponsor an international conference that brings together 10 young career scientists in the network to highlight the advances of these investigations and identify the outstanding scientific questions.



Above: Collection of fresh snow samples at Storm-Peak Laboratory, Steamboat Springs, Colorado. [Brent Christner, Louisiana State University]



Above: An autonomous unmanned aerial vehicle (UAV) during flight at Virginia Tech's Kentland Farm in Blacksburg, VA. The UAV is equipped with a series of devices mounted under the wings to sample microorganisms in the lower atmosphere. [David Schmale, Virginia Tech]



Above: A cell of the ice nucleation active bacterium and plant pathogen *Pseudomonas syringae* as seen under transmission electron microscopy. The cell is about 1 μm long. [Cindy E. Morris, INRA, France]



Above: Spring frost on weeds in a tomato field. Ice formation on leaves at warm temperatures (about 4° C) is likely due to ice nucleation active bacteria that grow on the leaf surface. [C.E. Morris, INRA, France]

US-BIOTA-Sao Paulo: Assembly and evolution of the Amazonian biota and its environment: An integrated approach

Joel L. Cracraft, American Museum of Natural History (NSF 1241066); Christopher W. Dick, University of Michigan (NSF 1240869); Robert P. Guralnick, University of Colorado (NSF 1241029); Kenneth E. Campbell, LA County Museum of Natural History (NSF 1241042); Andrew V. Brower, Middle Tennessee State University (NSF 1241056); John M. Bates, Field Museum of Natural History (NSF 1241075); Barbara M. Thiers, Scott Mori, New York Botanical Garden (NSF 1241127)

This project seeks to understand the evolutionary and ecological history of Amazonia, one of the most diverse ecosystems on Earth. A goal of the project is to build a comprehensive database of plants and vertebrates, which, together with phylogenetic and phylogeographic analyses, remote sensing, geology, and Earth-systems modeling, will be used to understand how the Amazonian biota was assembled across space and time.

Amazonia is Earth's most iconic center of biological diversity and endemism. It includes a vast landscape of lowland rainforest in Brazil, Peru, Colombia, Ecuador, Bolivia, and

Venezuela. It harbors the world's highest species diversity, the largest fresh-water ecosystem in the world, and contributes substantially to shaping the Earth's atmospheric gasses and oceans and consequently its climate. Despite this global importance, we do not fully understand how this biodiversity-rich biome developed over time. Knowing that history is crucially important for understanding how the short and long-term effects of biodiversity loss and climate change will impact the region, and the globe. This project seeks to answer an overarching question in biodiversity science: How was the modern Amazonian biota and its environment assembled across space and time?

The research is designed to understand the evolutionary and environmental-ecological history of Amazonia over the past 10 million years through a comparative approach that integrates systematic biology, population biology, ecosystem ecology, geology, Earth systems modeling and remote sensing, and paleoenvironmental history. The project involves researchers from seven research institutions in the United States, one in Canada, two in Great Britain, six institutions and universities in Brazil, and two in Argentina.

The project will be the most integrative study of Amazonian biodiversity and its history to date. The research team will build the largest database for Amazonian plants and vertebrates, use genetic data to reconstruct the temporal development of Amazonian species diversity, employ geological field methods to develop a more detailed understanding of the history and change in the Amazon's major river systems, and then integrate these findings with climate and atmospheric modeling to describe how Amazonia's ecosystems have affected global systems over time. In doing this research, the project will establish a methodological template for analyzing information about the history of biotic and environmental change across large, ecologically complex landscapes.

The project creates a large framework for formal and informal education including the training of students, development of a major museum exhibit on Amazonia, workshops for K- 12 STEM teachers, publications in professional educational journals, and a web portal, *The Evolutionary Encyclopedia of Amazonian Biodiversity*, that will make all results available to the public, as well as serve as an informational platform about Amazonian biodiversity and its global importance.



Left: Amazonian forest biomass stores ~86 Pg of carbon and >300g m⁻² of nitrogen. They also contribute ~20% of atmospheric O₂ and 10% of global terrestrial NPP. How patterns of these flows changed in the late Neogene will be addressed by this project [Joel Cracraft, American Museum of Natural History]



Above: Flowers of *Lecythis persistens*, a species of the Brazil nut family, an Amazonian group that co-evolved with its pollinators which are mostly bees, but also include bats [Scott Mori NY Botanical Garden]

Above right: Hoffmann's two-toed Sloth (*Choloepus hoffmanni*) is distributed in rainforests of lower Central America, northwestern South America, and western Amazonia. Usually hidden in the canopy during the day, they eat vast quantities of leaves at night and slowly digest them with the aid of symbiotic bacteria. [J. Cracraft]



Above: Widely distributed in tropical American forests the orchid *Prosthechea fragrans* is a common cultivar [J. Cracraft]



Above: Widely distributed within northern Amazonian rainforests, the collared puffbird (*Bucco capensis*) sallies for insects from hidden perches in the forest [John Bates, Field Museum of Natural History]

Below: The wetlands of Amazonia is home to the largest rodent in the world, the Capybara (*Hydrochoerus hydrochaeris*), which can weigh as much as 150 pounds (66 kg) [J. Cracraft]



Do parallel patterns arise from parallel processes?

Michael N. Dawson, J. Michael Beman, University of California, Merced (NSF 1241255); Julian P. Sachs, University of Washington (NSF 1241247)

This project will examine the current and historical diversity in marine lakes that formed as melting ice sheets raised sea level. Many of these lakes were isolated from each other, providing opportunities for species in the lakes to evolve independently under similar environmental conditions.

We will examine the extent to which communities of marine microbes, algae, invertebrates, and fishes in a suite of ‘natural experiments’ are influenced in similar or divergent ways by factors including environmental change.

The ‘natural experiments’ we study have been running for many thousands of years in marine lakes. Marine lakes formed as melting ice sheets raised global sea level >100 m after the last glacial maximum, inundating coastal valleys and creating hundreds of marine lakes worldwide. Dozens are found in close proximity in several locations in the Indo-West Pacific region, and our focus is on exemplars in Indonesia and Palau; the latter includes the most famous marine lake, ‘Jellyfish Lake’, which holds millions of jellyfish of a subspecies found nowhere else in the world.

The island-like marine lake habitats were inoculated with marine life from the surrounding sea as they flooded, and then became isolated to varying degrees for the next 6,000-15,000 years – providing multiple, millennia-long, independent evolutionary ecological experiments. The long history of each lake – during which organisms colonized the lakes, populations waxed and waned, species changed and some were extirpated and perhaps replaced – was recorded in sediments deposited on the lake bottom. By coring down through these sediment layers we will examine how environmental conditions and the species inhabiting each lake varied through time and led to the modern marine lake

communities we see today. Through species surveys, DNA sequencing, biogeochemical analysis, and modeling, we will explore the extent to which deterministic (e.g. selection) and stochastic (e.g. drift) processes collectively influence the diversity of species, genes, and function – and their interactions. The project examines the underlying processes that assemble and influence ecosystems, and asks whether these processes extend across different types of diversity (i.e. genes, species, and ways of living), different domains of life, and between land and sea.

The project will support more than a dozen early career scientists, from undergraduate students to a postdoctoral researcher, including student groups promoting scholarship, professional development, and evidence-based public education. With colleagues at other institutions, we will study fossil DNA, develop physical and digital collections, and incorporate project data into a general framework for community ecology and biogeography. The research directly contributes baseline surveys of biodiversity in ecosystems that may become heavily used for tourism in the coming decade in West Papua, and contributes to ongoing assessment and protection of a newly inscribed World Heritage Site in Palau. Project PIs will work closely with government and non-government conservation and education groups, and with dive and tour guide businesses, to raise awareness of biodiversity value and threats in Indonesia and Palau.



Above: The planktonic community of Ongeim'I Tketau, also called 'Jellyfish Lake', includes millions of the endemic jellyfish *Mastigias papua etpisoni*. [Michael N Dawson, UC Merced]



Above: *Mastigias papua* medusa morphology in the ocean (left) and five marine lakes. Images of marine lake medusa are organized (from second left to far right) by increasing duration of isolation from the ancestral ocean population. [Michael N Dawson, UC Merced; Patrick Colin, Coral Reef Research Foundation]

The animal host as an engine of microbial diversity: Evolutionary pattern and ecological process shaping the gut microbiota of *Drosophila* species

Angela E. Douglas, Gregory Loeb, Cornell University; John Jaenike, University of Rochester (NSF 1241099)

This project will examine the microbial communities in the gut of fruit flies to understand how the fruit fly hosts and bacteria influence each other, and how this type of interaction may contribute to the process of evolution of hosts and the diverse assemblages of microbes that live within them.

Almost all animals are chronically infected with a diverse assemblage of bacteria, most of which are beneficial or harmless. The cooperative relations between animals and their resident bacteria are believed to make a crucial contribution to global diversity by promoting the evolution of new species and novel biochemical and physiological functions. Until recently, our understanding of the significance of such mutually-beneficial interactions has been constrained by uncertainty about the relationship between the tally of bacterial species present (taxonomy) and what they are actually doing (function) within their animal hosts. Recent advances in molecular biology and genomics, however, have revolutionized our capacity to understand the linkage between taxonomy and function.

Fruit flies and their relatives provide an especially amenable system to investigate this relationship because the new genomic tools can be combined with information from a century of genetical research on fruit flies. In this project, we will apply molecular measures of diversity to investigate how the function of bacterial communities in fruit flies can be predicted from their taxonomic composition, and how these properties of the bacterial communities are influenced by the fruit flies in which they reside. In this way, we will gain a first insight into the significance of animal hosts as drivers of microbial diversity. We will also investigate the

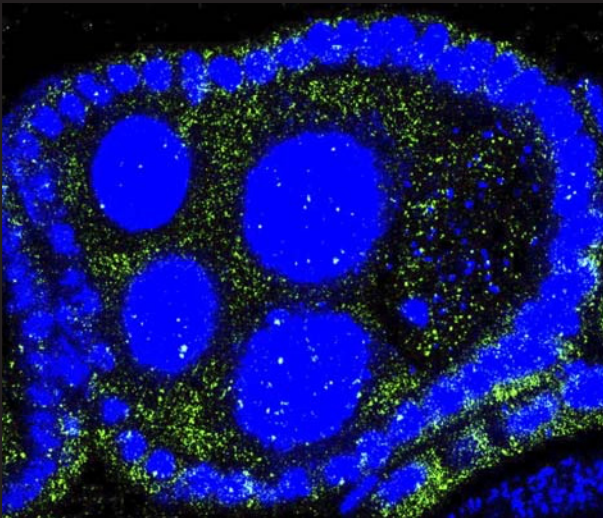
reciprocal process: how interactions with the bacteria affect various traits of the animal host, including food processing, habitat choice, competition, and interactions with parasites, all of which can potentially drive animal diversification. This research on animal-microbial associations will provide answers to the important scientific questions about the significance of mutually-beneficial interactions in shaping the taxonomic and functional diversity of organisms. The project will provide research training to two postdoctoral associates, a graduate student and undergraduate research assistants. The research team will interact with various audiences to promote an appreciation and understanding of biodiversity, at scales from an individual human body to the global biosphere. We will conduct talks and hands-on demonstrations at Science Saturday meetings for the general public, and organize a photographic exhibition communicating the beauty, complexity, and diversity of animal-microbial associations, also open to the general public. In parallel, lectures and discussion sessions with groups of school teachers conducted under the auspices of the Cornell Institute of Biology Teachers will assist teachers in delivering biodiversity concepts to the classroom, and we will interact directly with schools through various routes, including the Birds, Bugs and Books Literacy Program.



Above: *Drosophila suzukii* on raspberry
[H. Burrack, North Carolina State University]



Above: *Drosophila melanogaster* gut dissected from an individual that fed on a diet with 0.25% phenol red. The alkaline region of the gut is stained red (distal midgut), and more proximal and acidic regions are stained yellow.
[Angela Douglas, Cornell University]



Above: Micrograph of Wolbachia (green) associated with the egg chamber of a *Drosophila neotestacea*.
[Jeremy Herren and John Jaenike, University of Rochester]

Community assembly and decomposer function of aquatic fungi along a salinity gradient

Astrid Ferrer, James Dalling, Katy Heath, University of Illinois Urbana Champaign (NSF 1241212)

Diverse groups of freshwater and marine fungi remain to be described from tropical waters. This project will look at the role that these aquatic fungi play in the decomposition of wood along salinity gradients in coastal rivers in Panama.. A goal of the project will be to determine how gene expression patterns among these diverse fungi influence the rate and trajectory of wood decay in water

Wood washed into streams and rivers is an important source of energy for freshwater and estuarine food webs. Aquatic fungi, a diverse group of decomposer organisms adapted to life in water, play a key role in wood decay because they can both penetrate wood and produce enzymes which breakdown complex wood polymers. The goals of this project are to understand how aquatic fungal communities assemble, to determine which enzymes these fungi use to degrade wood, and to explore how a gradient of salinity from freshwater and estuarine environments impacts both fungal species composition and rates and processes of decomposition.

A wood decomposition experiment will be replicated in three pristine river systems in Coiba Island National Park on the Pacific coast of Panama. Replicate wood blocks will be placed at sites across stream to estuary salinity gradients and allowed to decompose for as long as two years. After removal from the water, wood blocks will be sampled for fungi using classical approaches (e.g., isolation and morphological description of fungal spores and fruiting bodies) and gene sequencing to identify fungi that cannot be grown in culture. This study will also link fungal community composition to the process of wood decay. Sub- samples of each wood block will be used to determine how wood chemistry changes during decomposition, and RNA will be directly extracted from wood to target the expression of genes associated with the production of wood decay enzymes. Collectively, these data

will be used to test the hypothesis that marine and freshwater fungal lineages possess different functional genes resulting in distinct decay trajectories that diverge through time. Our understanding of the evolutionary relationships of aquatic fungi is far from complete. Recent sampling in Central and South America (the Neotropics), indicates that new species, genera, and families of these fungi remain to be described. This project will contribute to our understanding of the taxonomy of aquatic fungi, and their evolutionary relationships with their terrestrial counterparts. An improved understanding of how aquatic fungi degrade the most recalcitrant structural components of wood (cellulose and lignin) may also reveal novel classes of wood- decay enzymes that can be used in the processing of biofuels and for bioremediation. Aquatic fungal are also known to be rich in anti- microbial compounds with potential for novel drug development. Fungal cultures collected through this work will therefore be provided to an existing bio-prospection project based in Panama. This research will provide training at the undergraduate, graduate, and post-doctoral levels in diverse disciplines ranging from ecosystem ecology to fungal taxonomy and bioinformatics. Research results will be communicated broadly via a bilingual website, through activities and public lectures hosted by the Smithsonian Tropical Research Institution Office of Education, and through workshops in fungal taxonomy and ecology offered to US and Panamanian students.



Above: Mouth of the Boca Grande River, Coiba Island, Panama. Aquatic fungi will be studied at this site and at two other undisturbed rivers. [Kevan Mantell]



Above: Aquatic ascomycete, *Luttrellia halonata*, showing an ascospore surrounded by a mucilaginous sheath. [Astrid Ferrer]



Above: Mitosporic fungus, *Flabellospora multiradiata*, with conidia adapted to aquatic habitats. [A. Ferrer]

A community level approach to understanding speciation in Hawaiian lineages

Rosemary G. Gillespie, John Harte, Rasmus Nielsen, Patrick O'Grady, University of California Berkeley (NSF 1241253); Daniel S. Gruner, University of Maryland (NSF 1240774); Kerry L. Shaw, Cornell University (NSF 1241060); Donald K. Price, University of Hawaii (NSF 1241228)

This project will examine arthropod communities on two Hawaiian islands to understand patterns and rates of evolution. The two islands differ in age, providing an opportunity to study evolution in multiple lineages in different ecological contexts.

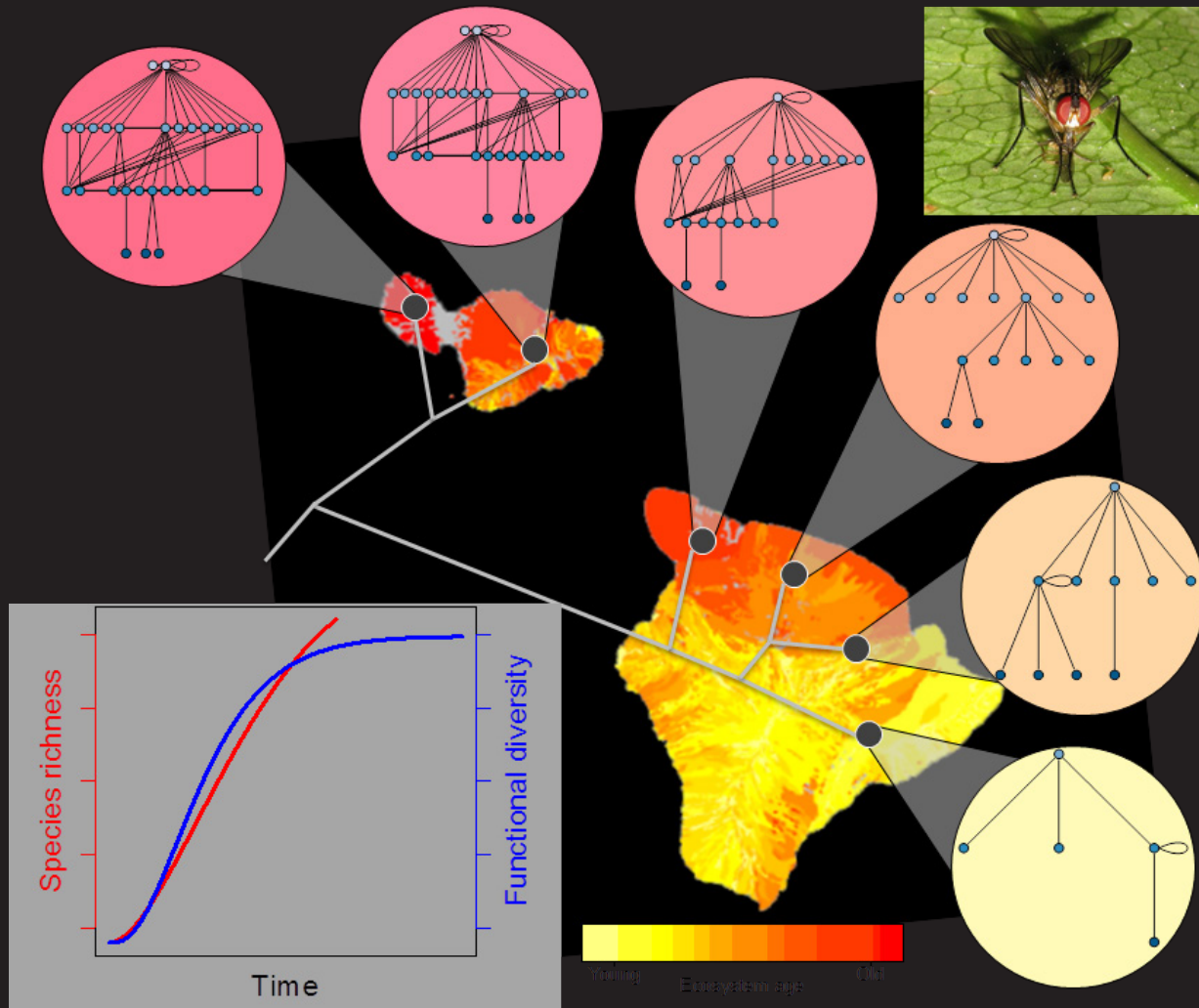
Our goal is to merge two disparate areas of research to understand patterns of biodiversity, (1) a broad ecological approach which provides insights into how species come together and interact in a community though focusing on locations at one point in time; (2) a lineage based approach which focuses on how species adapt, multiply, or decline over time, but cannot incorporate community parameters and interactions.

The first approach allows insights into whether patterns of biodiversity are predictable, by focusing on diversity and abundance of species at a site and the kinds of predator-prey or other interactions between species. The second approach allows assessment of the rate at which a given lineage of organisms can adapt and diverge, and changes in abundance as it does so.

We have an extraordinary opportunity to integrate these two approaches by using a system of age-structured biological communities in the youngest island of Hawaii and comparing these to communities on the next older island of Maui. Within Hawaii Island, lineages of organisms are actively diversifying, while the community and food web contexts in which they are embedded are changing with the development of their habitats. The system is relatively simple ecologically, but importantly it represents an environmental chronosequence, allowing for a 'space-for-time' substitution. Thus,

variables relevant to entire communities can be measured at multiple "slices in time" over the period of community formation, while assessment of population histories and dynamics over the same landscape allows insights into how the organisms within these sites have adapted, changed, and formed new species, in the context of other organisms in the community.

We will focus on 11 sets of arthropods that differ in terms of their role in the community (predator, herbivore, detritivore) and are each known to have diversified across the island chronosequence. We will then (1) determine how each of the 11 sets has changed in diversity, abundance, and interactions with others in the community at the different time slices; and (2) using molecular genetic approaches, assess the evolutionary history of changing abundance, adaptation, and speciation, over the same time period. By showing the importance of priority, sequence, and associated interaction strengths among members of a community on how biodiversity is generated, assembled, and lost, the work will provide answers to questions as to what are the impacts of biological invasions in a community, how do we establish successful conservation management practices in the context of changing ecosystems, and how can we develop effective programs in restoration ecology.



Above: A Hawaiian carnivorous caterpillar, *Eupithecia palikea*, feeding on a fruit fly. The two rearward pointing hairs on the green caterpillar are the triggers that cause it to snap around and grab its prey. [Karl Magnacca]

Above: Predicted changes in food webs across the geological age structure on two islands, Hawaii (larger) and Maui. Food webs (within colored circles) are expected to increase in complexity with time, as are species richness and functional diversity (lower left). Branching lines connecting sample sites are hypothetical phylogenetic (phylogeographic) relationships among taxa at those sites [Andrew Rominger]. Inset at upper right is a predatory fly, an example of a focal taxon in many of these food webs [Karl Magnacca]

The taxonomic, genomic, and functional diversity of soil carbon dynamics

Bruce A. Hungate, James Caporaso, Paul Dijkstra, Jane Marks, Egbert Schwartz, Northern Arizona University (NSF 1241094); Lance Price, Translational Genomics Research Institute (NSF 1241115)

This project will examine the roles that taxonomic and genetic diversity of microbes play in the processing of new and old carbon in soils.

Microbial diversity is vast, and recent discoveries place soils as home to the most diverse of the Earth's microbial communities. The current project will probe a surprising response of microorganisms to changes in soil carbon availability: when new carbon enters soil, especially carbon that is easily assimilated and decomposed by soil microorganisms, a chain reaction occurs leading to the breakdown of older soil carbon, carbon that would otherwise have remained stable. Current theory does not explain this chain reaction. This project will test whether taxonomic biodiversity and the genetic biodiversity it supports – in other words, who is there and what are they doing – can explain this unusual carbon cycling phenomenon. Researchers will use long-term study sites in soils spanning a climatic gradient in Arizona and a variety of molecular, genomic, chemical and analytical approaches. The work will test the idea that parts

of the carbon cycle are emergent consequences of interactions among organisms, with biodiversity as a fundamental driver, thereby connecting genes to communities to ecosystems.

The proposed work addresses important questions both in biodiversity science and the global carbon cycle, and is important because soil carbon is a major reservoir, storing about three times the amount of carbon contained in the atmosphere as carbon dioxide. Microbial biodiversity is the biological template upon which much of the carbon cycle unfolds, yet evidence of how diversity alters the soil carbon cycle remains elusive. This project will address this fundamental knowledge gap, generate information applicable to carbon management, train new scientists at the undergraduate, graduate, and post-doctoral levels, and engage the public through outreach activities.



Above: Collecting soil for microbial diversity analysis [Paul Dijkstra, Northern Arizona University]



Above: Doctoral student Rebecca Mau processes DNA samples for stable isotope probing, a technique that identifies organisms responsible for particular functions in soil. [Paul Dijkstra, Northern Arizona University]

The role of taxonomic, functional, genetic, and landscape diversity in food web responses to a changing environment

Anthony R. Ives, Volker C. Radeloff, University of Wisconsin (NSF 1240804); Kerry M. Oliver, University of Georgia (1240892); Jason P. Harmon, North Dakota State University (NSF 1241031)

The project will examine how genetic, taxonomic, ecological, and landscape diversity influence the control of agricultural pests by their natural enemies.

The future of agriculture in the United States will face challenges presented by a changing climate. Our project will investigate the responses of agricultural pests and their natural enemies, as a model system to understand how food webs may respond to changing environments.

Many agricultural pests are kept in check by natural enemies – predators and parasites that suppress pest outbreaks. Promoting the success of these natural enemies is often a cost-effective and environmentally friendly approach to pest control. The changing climate, however, will shift the interactions between pests and their natural enemies in many possibly unforeseen ways. Higher temperatures might increase the population growth rates of pests (bad), or they might increase the predation rate of natural enemies (good). Climatic changes will also likely change the forces of natural selection acting on both pests and predators. The resulting evolution might increase the tolerance of pests to extreme heat events (bad), or it might lead to the greater vulnerability of pests to natural enemies (good). Given these numerous possibilities, anticipating changes to natural pest control in agricultural systems requires an understanding of the interplay between ecological and evolutionary forces in agricultural food webs. Such an understanding may also help to predict how changing environments will affect natural food webs.

Our research addresses how genetic, taxonomic, ecological, and landscape diversity affect the control of agricultural pests by natural enemies. The study will focus on three crops – corn, alfalfa,

and soybean – and the group of aphid species that attacks them. Aphids are normally kept in check by roughly 20 common natural enemies. Because these natural enemies move frequently among fields and other habitats, their ability to suppress aphids depends upon the diversity of the landscape. Furthermore, aphids contain bacterial symbionts that give their insect hosts tolerance to high temperatures. These symbionts thus make it possible for aphids to evolve rapidly in response to climate changes. How widespread and important these bacterial mutualists are among aphid species, and more broadly among other herbivorous insects, are unknown. Because they represent a possible “extended genotype” of insects, these symbionts could underlie the potential for rapid evolution to different environmental changes.

Our work will integrate information at the molecular level of the interacting genomes of aphids and their symbionts, at the ecological level of changing abundances of pests and their natural enemies, and at the continental scale at which regional adaptation through evolution will occur. Therefore, we need to employ molecular genetics, ecological sampling, and remote sensing from satellites. The proposed work will not only address the basic and applied scientific challenge of anticipating the consequences of climate change for agricultural pest control. It will also educate the public by enlisting the help of citizen scientists who will sample aphids and natural enemies across the USA, bringing hands-on science into citizen’s backyards.



Above: The multicolored Asian ladybeetle, *Harmonia axyridis*, was introduced into North America to control aphid pests. Unfortunately, although it does control some aphid species, it is itself a pest, attacking fruit crops in fall and sometimes nipping humans. [A.R. Ives]



Above: Pea aphids come in two colors controlled by a single gene, similar to eye color in humans. Because different colored lines of pea aphids contain different bacterial symbionts, we can use color as a marker to identify lines with different tolerance to high heat events. [A.R. Ives]



Above: The parasitic wasp *Aphidius ervi* was also introduced to control aphids, in particular pea aphids. It attacks aphids by injecting an egg into them. The egg then hatches and eats the still living aphid from the inside out. This type of parasitic wasp was the inspiration for the movie *Alien* and its sequels. [A.R. Ives]

The role of biodiversity for microbial adaptation to anthropogenic perturbations

Konstantinos T. Konstantinidis, James Spain, Eberhard Voit, Georgia Tech (NSF 1241046)

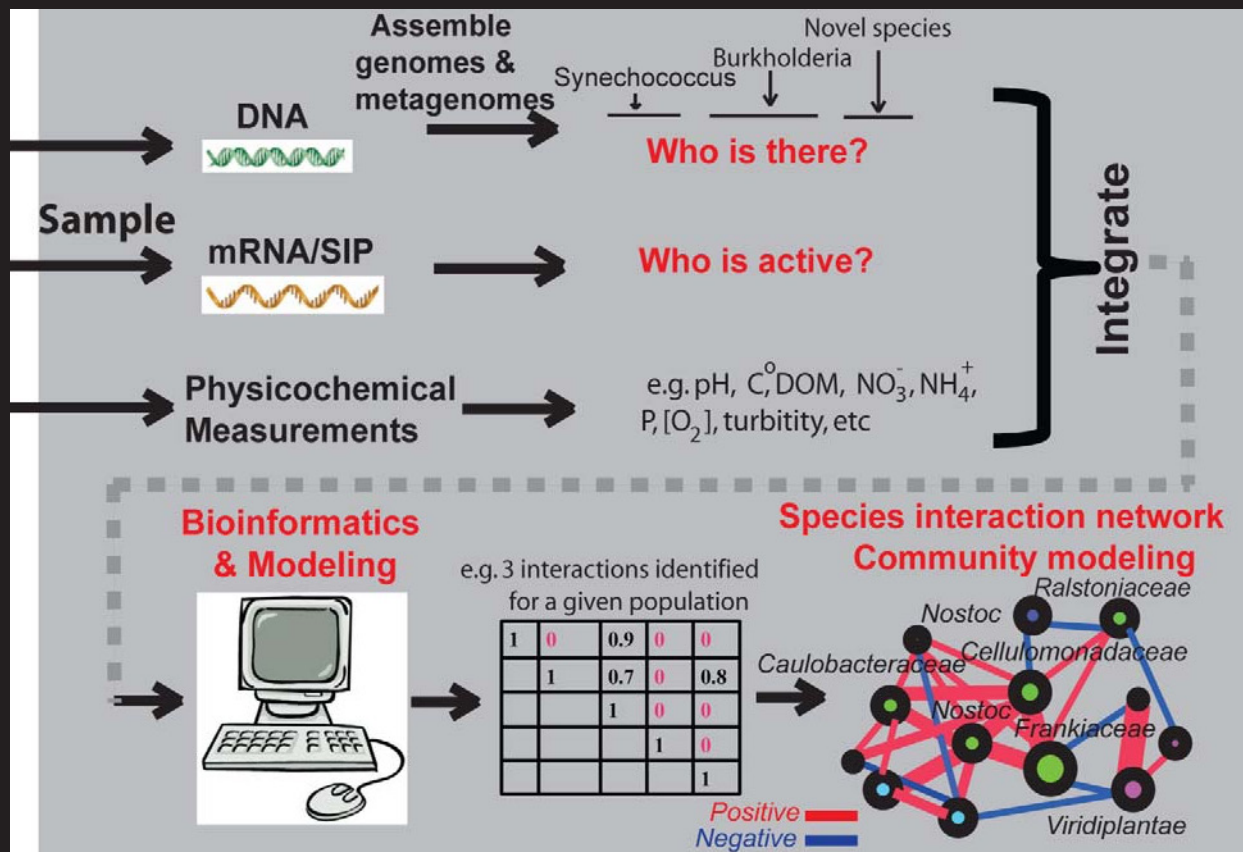
This project will examine how microbial species and communities respond to disturbance and to the presence of new organic compounds such as petroleum hydrocarbons, pesticides, and antibiotics.

A single liter of water or gram of soil contains hundreds, if not thousands, of bacterial and archaeal species, each of which typically makes up a very small fraction of the total microbial community (<0.1%) but all together constitute a substantial part of the community, sometimes >50% (the so called “rare biosphere”). The basis for – and the value of – this astonishing microbial biodiversity remain poorly understood, primarily due to the fact that traditional methods reveal the numerically dominant members of the community related to the flow of the major carbon and nitrogen sources. Yet, it is to be expected that the diversity of (rare) species found in a given habitat contributes substantially to community function and resilience, in particular by serving as a source of metabolic diversity and genomic innovation, and constitutes the evolutionary scaffold that shapes the responses to natural as well as anthropogenic fluctuations in the environment, including major perturbations such as global climate change. Therefore, central to a predictive understanding of the importance of microbial biodiversity for ecosystem function and for the process of adaptation is to obtain a more complete picture of the mechanisms by which low abundance genes and species contribute to community function. This project will employ advanced genomic techniques and mathematical modeling to explore how rare genes and species contribute to the process of microbial adaptation by determining

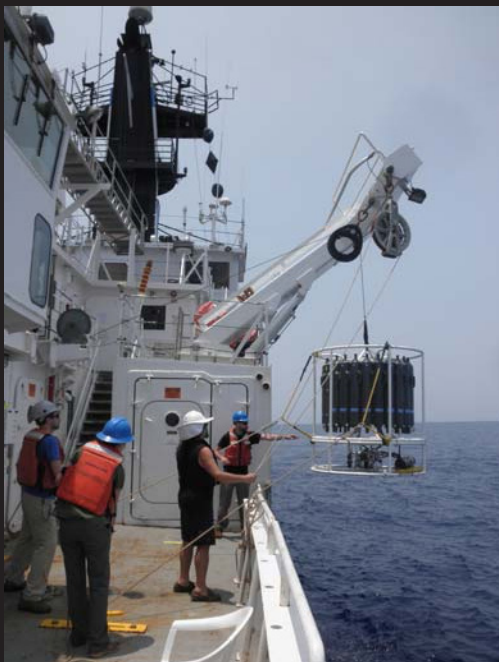
the molecular adaptations that occur in a complex community upon the addition of a new organic compound or the occurrence of an environmental perturbation such as a storm event. The organic compounds will include important environmental pollutants such as petroleum hydrocarbons, pesticides and antibiotics.

The response of the microbial communities will be evaluated in both well-defined laboratory mesocosms as well as natural microbial communities of important freshwater and marine ecosystems of the Southeast USA. Thus, the expected findings will have important biotechnological applications and health benefits related to the fate and biodegradation of the above compounds and will lead to a more predictive understanding of the role of microbial biodiversity for ecosystem function and resilience to natural and anthropogenic perturbations.

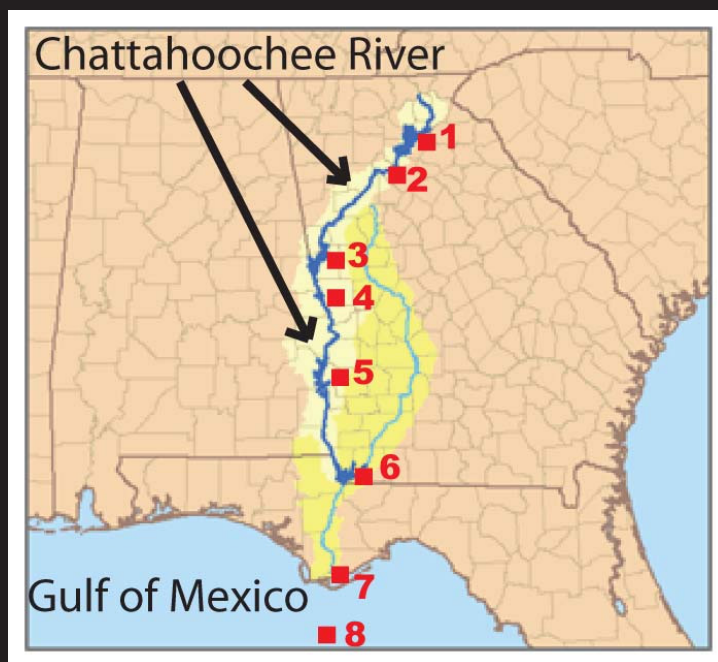
New multi-disciplinary technologies to assess the roles of yet-to-be-cultured microorganisms will be developed and made publicly available. Graduate and undergraduate students, including at least five minority students from the University of Puerto Rico, Mayaguez, will be trained at the interface of microbiology, computational systems biology and engineering, a pivotal, interdisciplinary area of contemporary research that is not adequately covered in traditional academic settings.



Above: A schematic overview of some of the approaches that will be employed in this project. [K.T. Konstantinidis]



Above: Sampling in the Gulf of Mexico. [K.T. Konstantinidis]



Above: Map of sample locations along the Chattahoochee River.

Historical and contemporary influences on elevational distributions and biodiversity tested in tropical Asia

Thomas E. Martin, Robert Fleischer, Ellen Martinsen, University of Montana (NSF 1241041); Frederick H. Sheldon, Louisiana State University (NSF 1241059); Robert G. Moyle, University of Kansas (NSF 1241181)

This project will examine multiple factors that may contribute to the maintenance of elevational gradients in biodiversity, using a diverse tropical bird fauna in Borneo.

Causes of latitudinal and elevational gradients in biodiversity remain a major scientific challenge. We outline traditional (physiological tolerance, competition, opposing boundaries) and novel (taxon age, adult survival, life history traits) hypotheses and integrate them with dispersal, genetic structure, and evolutionary history to provide a conceptual framework that has the potential to yield major advances in theory and understanding across disciplines. An early hypothesis for elevational zonation and adjacent distributions of related species was predicated on climate stability and a relationship between physiological tolerance and dispersal. This hypothesis has major ramifications for speciation, genetics, ecology, and evolution, but there has not been a strong test of the relationship between physiological tolerance and dispersal. Others have argued that biotic interactions, like competition, are more important in defining boundaries. Contradictory evidence exists, and direct tests of the interacting and contrasting roles of physiological tolerances versus competition on range boundaries, dispersal, and genetic structure are needed. Life history traits (e.g., development rates, parental care, longevity, extra-pair mating) may interact, but have not been considered. We propose alternative hypotheses for the potential interaction of an elevational climate gradient, physiological tolerance, competition and life history traits on dispersal propensity and genetic structure, and the consequences for diversification and community structure. Testing these hypotheses simultaneously has the potential

to yield truly transformative advances in theory. Elevational zonation of related species and diversity gradients are strongly expressed in tropical organisms, particularly tropical songbirds. We will examine an elevational gradient of tropical birds in Asia, where functional, genetic, and phylogenetic diversity of organisms are woefully understudied and underlying patterns provide a strong system for testing these hypotheses. We will characterize bird species richness and community composition in Bornean for two of the most diverse superfamilies in Asia. We will examine physiological tolerances of embryos and adult birds to variation in temperature, and test the role of competition using playback experiments. Those results will then be integrated with data on dispersal obtained from genetic and capture/recapture methods.

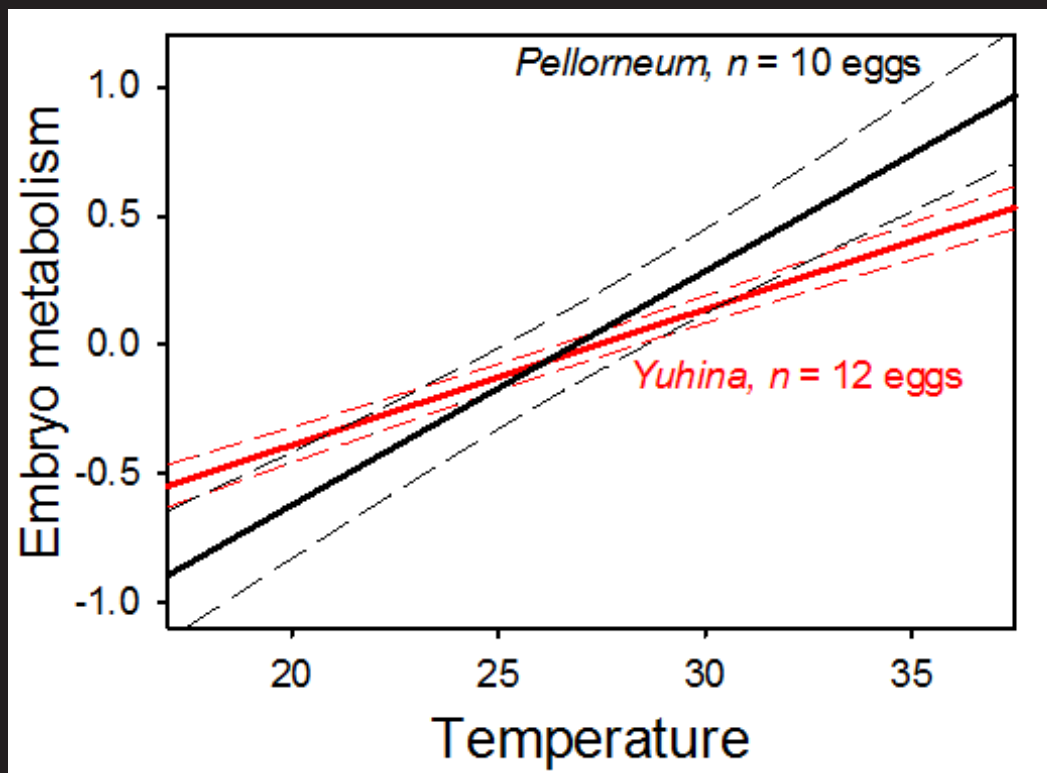
The proposed work will provide extensive opportunities to train graduate and graduate students, and provide unique opportunities for cross-disciplinary training and cross-cultural life experience. Public outreach will be achieved by working with high school students and teachers, developing exhibits at the Smithsonian, and production of an educational video on tropical bird nesting behaviors. Finally, this project has critical conservation ramifications, as tropical Asian forests are being lost more quickly than any other tropical forests, and our work will provide critical information on possible vulnerabilities to climate change.



Above: *Pellorneum*, an endemic species in Borneo, standing at its nest entrance, has a narrow elevational distribution, potentially associated with the greater sensitivity to temperature of its embryos. [T. E. Martin]



Above: *Yuhina*, an endemic species in Borneo, has a wide elevational distribution, potentially associated with the lower sensitivity to temperature of its embryos. [T. E. Martin]



Above: Embryo metabolism, corrected for embryo age and mean species differences, relative to temperature. The steeper slope of *Pellorneum* shows its greater sensitivity to temperature. Dashed lines reflect 95% confidence intervals. [T. E. Martin]

Anthropogenic nutrient input drives genetic, functional and taxonomic biodiversity in hypereutrophic Lake Taihu, China

Hans W. Paerl, University of North Carolina (NSF 1240851); Wayne S. Gardner, University of Texas at Austin (NSF 1240798); Steven W. Wilhelm, University of Tennessee (NSF 1240870); Ferdinand L. Hellweger, Northeastern University (NSF 1240894)

This project will examine the species and genetic diversity of microbes in a lake that experiences massive blooms of toxic cyanobacteria, and link that diversity to the processing of nitrogen that is the cause of the toxic blooms.

The availability of clean, potable water remains one of society's greatest challenges, even within developed nations. Lake Taihu, the third largest freshwater lake in China, is the sole drinking water resource for some 10 million residents. Like lakes and rivers in North America and around the world, human activities have increased nitrogen inputs dramatically, causing algal blooms that threaten economic and recreational uses of those waters. Often, these blooms are dominated by cyanobacteria, which produce an array of secondary metabolites that are toxic to water users and consumers, including humans.

The identities, nitrogen processing capabilities, and activities of the cyanobacterial and associated microbial communities in Lake Taihu will be examined to determine if nitrogen processing rates in the lake water and sediments can be predicted from the phylogenetic identity and genetic makeup of those communities. Various components of the lake's nitrogen cycle will be measured and linked quantitatively to representative molecular markers. Coupled with high throughput genetic sequencing, these molecular markers will provide a genetic database of nitrogen-cycling processes in freshwater ecosystems.

A goal of the project will be to link microbial taxonomic, genetic, and functional data in a mechanistic mathematical model that describes the relationship between the existing community (diversity), the associated N cycling transformations (function), and

the distribution and abundance of functional genes and transcripts for signature processes (genetics). The genetic potential of the microbial community will be linked to ecosystem function through this modeling framework that predicts how reduction of nutrient inputs will affect toxic cyanobacterial bloom potentials in Taihu. This approach provides the capability for an ecosystem-scale systems biology approach to environmental management.

Lake Taihu will be a 'looking glass' for other large lake ecosystems worldwide that are threatened by proliferating toxic cyanobacterial blooms. The project will be broadly applicable to process-based management of aquatic systems experiencing excessive nutrient inputs. International (US-China) collaboration, education of 3 graduate, undergraduate (REUs from new UTK and UNC-CH sites) and secondary school students, training of a postdoctoral fellow and incorporation of science journalism students into field studies to promote adult scientific literacy are all components of our program involving five major US academic institutions. Recruitment of students through established and new programs will enhance participation of underrepresented groups. Student exchanges between Chinese (*Nanjing Institute of Geography and Limnology; Chinese Academy of Sciences*) and American institutions (*UNC-CH China Technology Learning Program*) will facilitate cultural and philosophical exchanges and provide valuable international research experience for students.



Sampling Lake Taihu, China. [H.W. Paerl, UNC Chapel Hill, Institute of Marine Sciences]

US-China: Disentangling the components of tree biodiversity: Integrating phylogenies, functional traits and transcriptomes

Nathan Swenson, Michigan State University (NSF 1241136)

This project will integrate genetic data with phylogenetic and functional trait approaches to the study of tree biodiversity, with the goal of developing a predictive framework that can be used to understand processes that generate and maintain forest diversity.

Temperate and tropical forests contain a significant proportion of our planet's biodiversity. This biodiversity plays a role in regulating the Earth's climate and provides crucial ecosystem services for our human population. Despite this importance, the processes that produce and maintain levels of biodiversity within and across forested ecosystems remain poorly understood. This lack of understanding not only applies to diverse tropical and subtropical forests, but also less diverse temperate forests. Further, the insights we do have primarily concern species diversity and far less is known about the processes regulating the phylogenetic, functional and genetic dimensions of biodiversity that are likely to be more closely related to ecosystem function.

Direct or indirect human impacts on forested ecosystems are widespread. Our ability to predict how forest biodiversity will respond to these pressures is limited by our understanding of the processes that underlie the structure and dynamics of biodiversity in forests. Increasingly ecologists have supplemented traditional approaches that examine only the species diversity in plant assemblages with analyses of multiple dimensions of biodiversity. For example, ecologists have now shown that phylogenetic and functional diversity are often better predictors of ecosystem function and community dynamics than species diversity. The existing difficulties with the phylogenetic and functional trait approaches to community ecology include the difficulty of mapping phylogenetic patterns to ecological processes and the ability of researchers to only quantify a few functional traits in even moderately

diverse communities. An increasingly feasible way to overcome these limitations is by integrating genetic diversity into this research program in the form of transcriptomics. Transcriptomes, the mRNA in a tissue, can now be quantified for non-model organisms and they provide a window into the aspects of the genome that are being transcribed (i.e. the functional genome).

We argue that integrating a large amount of detailed information, such as that provided by transcriptomes, into existing phylogenetic and functional trait based approaches could help overcome previous limitations. In other words, rapid advances can now be made that incorporate the genetic dimension of biodiversity with existing research on the phylogenetic and functional dimensions in diverse communities filled with non-model organisms. We expect that this approach will yield novel insights into the structure and dynamics of communities and improve our ability to predict the future of biodiversity.

This research program will bring together plant biologists from the United States and China to investigate the structure and dynamics of tree biodiversity in long-term forest dynamics plots in the USA and China. The team will design a novel approach in community ecology termed 'community functional phylogenomics' that aims to integrate phylogenetic, functional trait and transcriptomic diversity with patterns of species distributions, co-occurrence and dynamics.



Above: Understory of the Luquillo Forest Dynamics Plot in Puerto Rico. [Nathan Swenson, Michigan State University]



Above: The Gutianshan Forest Dynamics Plot in subtropical China that will be one of the forests studied in the research [Nathan Swenson, Michigan State University]



Above: *Miconia racemosa* seedling in the understory of the Luquillo Forest Dynamics Plot. [Nathan Swenson, Michigan State University]

Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity

Jonathan P. Zehr, Zbigniew Kolber, University of California Santa Cruz (NSF 1241221); Kevin R. Arrigo, Stanford University (NSF 1241093); Matthew Church, University of Hawaii (NSF 1241263)

This project will use genomics, molecular biology, and stable isotope tracers to investigate how changes in the form and availability of nitrogen affect taxonomic, genetic, and functional diversity of marine phytoplankton.

Marine phytoplankton (microalgae) are a diverse group of unicellular organisms that use photosynthesis to fix carbon dioxide into organic matter. They play important roles in controlling the gas composition of the atmosphere, they account for approximately 50% of global carbon dioxide fixation, and they are the base of the marine food web. Their growth is dependent on their ability to acquire the resources they need for growth. Nitrogen (N), an essential element for growth of all organisms, is found at extremely low concentrations throughout vast regions of the subtropical ocean, where N availability generally limits phytoplankton growth.

N in the ocean is present in multiple chemical forms, and phytoplankton have different capabilities for utilizing each form. The chemical forms and supply of N to phytoplankton have already been altered by anthropogenic activities, and increasing environmental perturbations will likely further enhance these alterations. Thus, changes in the amount of the different chemical forms of N, as well as the supply of N to the surface waters of the ocean where phytoplankton live, will likely lead to changes in the oceanic food web in future decades.

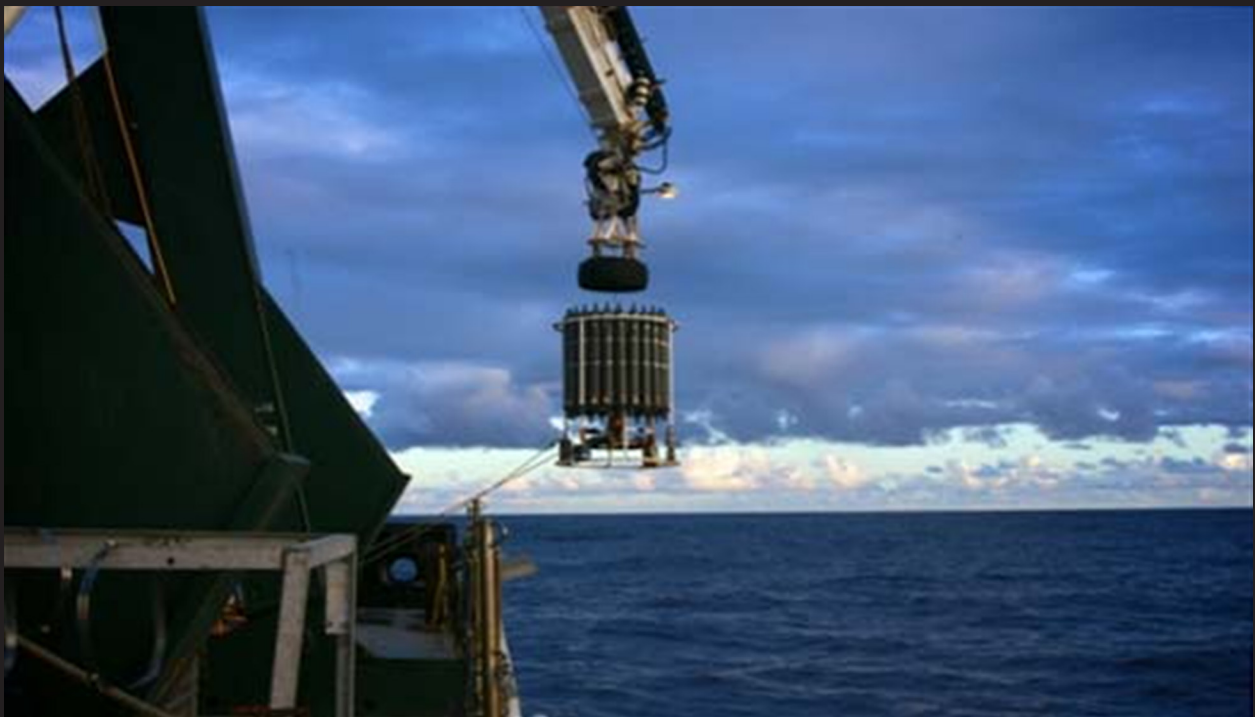
Therefore, it is critical to determine the links between the forms and fluxes of nitrogen in the ocean and the diversity of phytoplankton species.

Using new technologies for genomics, molecular biology, and stable isotope tracers, this project will investigate the effects nitrogen cycle perturbations have on the taxonomic, genetic, and functional diversity of marine phytoplankton communities in the nitrogen depleted Pacific Ocean, one of the largest biomes on Earth. The project will uniquely investigate community-to-single-cell level function and species (strain)-specific gene expression patterns that will provide new insight into how the intricacies of the marine nitrogen cycle control phytoplankton growth. This insight is fundamental for both predicting the effects global environmental change will have on marine ecosystems and informing future management of marine resources.

The project will engage students and postdoctoral researchers in state-of-the-art interdisciplinary research, spanning microbial ecology and genomics to oceanography and environmental science. Working with the well-known Exploratorium in San Francisco, California, students and postdoctoral researchers from the University of California, University of Hawaii and Stanford University will facilitate public dissemination of knowledge, by developing interactive displays focused on phytoplankton growth and genomics.



Above: Shipboard incubator tanks for experiments with phytoplankton communities under controlled conditions. [Sasha Tozzi, UC Santa Cruz]



Above: Deployment of a 'CTD rosette' off the stern of the research vessel Kilo Moana in the North Pacific Subtropical Gyre. This valuable tool contains bottles that can collect water at specified depths and sensors to measure conductivity, temperature, and depth. [Kendra Turk –Kubo, UC Santa Cruz]

Diversity and symbiosis: Examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota

Lisa K. Belden, Leanna L. House, and Roderick Jensen, Virginia Polytechnic Institute and State University (NSF 1136640); Reid N. Harris, James Madison University (NSF 1136602); Kevin P. Minbiole, Villanova University (NSF 1136662)

All animals host internal and external symbiotic microbes; most cause no harm and many are beneficial. This project will investigate the diverse microbial communities on the skin of amphibian species and their role in controlling a critical disease that threatens amphibian biodiversity in the Neotropics.

In humans, symbiotic microbes outnumber human cells ten to one. Most of these microbial symbionts are not harmful and many species are beneficial. The composition of these microbial communities can influence the likelihood that pathogens are able to successfully establish themselves in the body, how quickly toxins are metabolized and even whether individuals are lean or obese. Amphibians also possess a diverse symbiotic microbiota. Recent research suggests that the bacterial symbionts on the skin of amphibians may limit infection by pathogens, such as the chytrid fungus *Batrachochytrium dendrobatidis* that has decimated many natural amphibian populations around the globe.

But how do these diverse microbial communities of vertebrates achieve beneficial functions? Can microbial communities of varying species composition perform the same disease resistance function or is the presence of specific mutualists critical in disease resistance? Does the presence of a virulent pathogen like the chytrid fungus drive selection of the bacterial symbiont community based on critical functions, such as the ability to produce anti-fungal metabolites? This research project will address these questions by examining links between three critical diversity components of the symbiotic microbial communities that reside on amphibian skin: taxonomic diversity (number and

relative abundance of species), genetic diversity (which microbial genes are activated), and functional diversity (disease resistance). Using focused field surveys and manipulative experiments, three objectives will be addressed: (1) establish the range of taxonomic, genetic, and functional diversity within the microbial community on five amphibian host species in Panama, (2) examine how the presence of the fungal pathogen *Batrachochytrium* impacts diversity components, and (3) examine the relationship between microbial diversity and resistance to disease. As all animals host symbiotic microbes, these results will have broad applicability to other systems, including humans. In addition, new statistical methods for these complex datasets will be developed, which will rapidly expand the ability to integrate these diversity components in a wide array of systems. A partnership with the Panama Amphibian Rescue and Conservation Project (PARC) will also be established. A PARC intern will be supported to work with school groups to stress the importance of conservation, beneficial microbes, and biodiversity. The partnership with PARC will extend to working with them on novel probiotic solutions, based on antifungal skin bacteria, that will allow successful reintroductions of threatened frogs, such as the Panamanian golden frog, thereby helping to restore biodiversity to the Neotropics.



Brian Gratwick, Smithsonian Conservation Biology Institute



Jenifer Walke, Virginia Tech

Above: The red-eyed treefrog, *Agalychnis callidryas*, is found in Panamanian rain forests. The skin bacteria from this species and four additional species will be studied to determine how diverse communities of microbes provide protection from a lethal skin fungus (*Batrachochytrium dendrobatidis*).

Left: The bacterial species *Lysobacter gummosus* (lower streak) is found on amphibian skins and is shown inhibiting *Batrachochytrium dendrobatidis* (light colored lawn on the agar plate). The bacterial species at the top of the plate is a control that does not inhibit fungi.

Below: Panamanian frogs will be studied in rainforest habitats such as this that vary in exposure to *Batrachochytrium dendrobatidis*.



B. Gratwicke

Integrating genetic, taxonomic, and functional diversity of tetrapods across the Americas and through extinction risk

Thomas Brooks, Gabriel C. Costa, and Bruce Young, NatureServe (NSF 1136586); Catherine Graham, State University of New York, Stony Brook (NSF 1136705); Stephen B. Hedges, Pennsylvania State University, University Park (NSF 1136590); Volker C. Radeloff, University of Wisconsin, Madison (NSF 1136592)

Most large-scale efforts to assess biodiversity have focused on genetic, taxonomic, and functional dimensions individually; it is currently unknown how these dimensions relate to each other over space. Brooks and colleagues will use a database of the 13,000 land vertebrates of the Americas to consider how changes in one dimension of biodiversity influences changes in others. Understanding how species composition influences the diversity of functional traits, for example, will improve the efficiency and effectiveness of conservation actions.

This project will examine continent-wide variation in the dimensions of biodiversity. New data will be collected on the biodiversity and extinction risk of 2,500 Western Hemisphere reptile species. These data will be combined with existing data for mammals, birds, and amphibians to measure and map the diversity of all 13,000 terrestrial vertebrate species of the Americas, in three dimensions. The first is phylo-temporal diversity, measuring the genetic distinctiveness of the species in an area. The second is compositional diversity, measuring which species occur in an area. And the third is trait diversity, measuring how the species in an area vary in place, food, time, and size niches. For each of the three dimensions, measures will reflect differences over space (dissimilarity). All data will be published in open access databases. The research is important scientifically because it will be a novel, hemi-

sphere-wide analysis of the genetic, taxonomic, and functional diversity of a major species group. This will allow determination of relationships among the three dimensions of biodiversity, and, by using the extinction risk data, prediction of impending changes in these relationships. Understanding how these dimensions covary will improve the efficiency and effectiveness of conservation actions.

The PI institutions comprise four universities and the non-governmental organization NatureServe. The latter will provide a channel for incorporation of results into conservation decisions, as well as real-world exposure to the two postdoctoral associates, three graduate and approximately 40 undergraduate students that will be involved in the project.



Geoffrey A. Hammerson



G.A. Hammerson



G.A. Hammerson

Above left: *Gambelia wislizenii*, long-nosed leopard lizard (USA: Colorado)

Above center: *Crotaphytus collaris*, Eastern collared lizard (USA: Colorado)

Above right: *Aspidoscelis sexlineata*, six-lined racerunner (USA: Colorado)

Below left: *Rhinocheilus lecontei*, long-nosed snake (USA: Colorado)

Below right: *Opheodrys vernalis*, smooth greensnake (USA: Colorado)



G.A. Hammerson



G.A. Hammerson

Below left: *Agkistrodon contortrix*, copperhead neonate (USA: Connecticut)

Below center: *Amblyrhynchus cristatus*, marine iguana (Ecuador: Galapagos Islands)

Below right: *Sphaerodactylus copei*, Haitian big-scaled sphaero (Haiti)



G.A. Hammerson



G.A. Hammerson



S. Blair Hedges, Penn State University

Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts

Jed A. Fuhrman, David A. Caron, John F. Heidelberg, William C. Nelson, and Fengzhu Sun, University of Southern California (NSF 1136818)

Fuhrman and colleagues will compare heavily disturbed harbor regions and relatively pristine ocean habitat in the Los Angeles basin to better understand links between marine microbial diversity and ecosystem function.

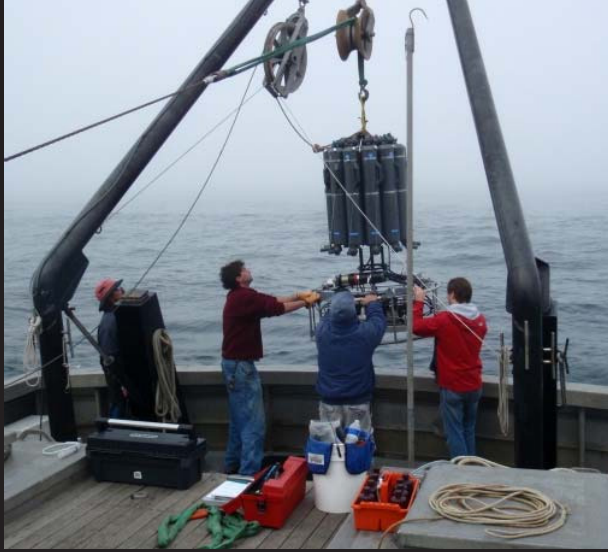
Bacteria, Archaea, and Protista dominate global elemental cycling and are immensely diverse genetically, taxonomically, and functionally. Yet the extent of marine microbial diversity, its patterns and relationships are very poorly characterized, even though the ocean covers 70% of the planet's surface. Among the least well known variables is the effect of human impacts on native marine microbial systems, although it is recognized that disturbed systems are more prone to events like harmful algal blooms. Knowledge of these relationships and impacts are necessary to anticipate the responses of biota to global changes and feedback mechanisms that may alter the extents, rates, and even pathways of such changes. This project expands upon an existing NSF-funded 10+-year monthly ocean time series (Microbial Observatory) to include quarterly sampling adjacent to the disturbed LA Harbor region and the barely-disturbed Santa

Catalina Island coast. The investigators will measure, 1) Genetic diversity: high throughput DNA sequences of "housekeeping" and functional genes; 2) Taxonomic diversity: high throughput tag sequences of small subunit ribosomal RNA genes, flow cytometry, automated image analysis; 3) Functional Diversity: a) Functional measurements (carbon fixation and respiration rates, microbial growth and grazing rates, cell size, morphology, and biomass variations), b) distribution and expression of target functional genes relevant to carbon, nitrogen, and sulfur cycles, c) evaluation of whole-community RNA to explore unanticipated

functionalities; 4) Integration will include: Multivariate statistical and network approaches including newly developed techniques (e.g. Bayesian networks to examine cause-effect relationships), and high speed computational approaches to assess the relationships among the genetic, taxonomic, and functional aspects of biodiversity observed. The researchers will also examine the data for signatures and specific effects (on organism identity and functions) associated with the disturbed site vs. the relatively pristine one.

This project offers an unprecedented and potentially transformative opportunity to combine and integrate measurements of genetic, taxonomic, and functional diversity along with direct measurements of system function in a well-studied marine system that includes a gradient from one of the world's busiest harbors to a largely pristine ocean habitat. Far beyond just describing the distributions of organisms and functions (itself a necessary first step), this project will specifically link spatial and temporal variations in a variety of functions with variations in genetic and taxonomic community composition.

The project will involve doctoral training of participants as well as a direct connection to K-12 education via the Centers for Ocean Sciences Education Excellence (COSEE) teacher training program at USC. Outreach will include an interactive website and direct interaction with the public at the Wrigley Marine Science Center.



Jed Fuhrman, University of Southern California



J.Fuhrman

Above left: Sampling for the San Pedro Ocean Time Series and the USC Microbial Observatory

Above right: Sampling from a small boat near Catalina Island

Right: An epifluorescence microscopy image of viruses (tiniest dots), bacteria (medium sized dots) and protists (larger ones) from the USC Microbial Observatory



J.Fuhrman

Below: Looking out to sea in the general direction of the USC Microbial Observatory from Catalina Island, near the USC Wrigley Marine Science Center



J.Fuhrman

Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, Inga

Thomas Kursar and Phyllis D. Coley, University of Utah (NSF 1135733)

This project will study interactions between members of the tree genus *Inga* (>300 species) and their insect herbivores at five sites in Central and South America. This work will shed light on the coevolution of plants and herbivores in the most diverse forest communities on Earth.

Tropical forests are extremely diverse, yet the factors that generate and maintain such high diversity are poorly understood. Over half of the species in tropical forests are plants and the insects that feed on them (herbivores), so examining these interactions may shed light on this long-standing puzzle. Plants have evolved a battery of defenses to protect their leaves from insects and insects are continually evolving counter-adaptations. Consequently, high rates of defense evolution may contribute in important ways to the origin of new species.

This research will explore how herbivores drive the evolution of plant defenses, how plant defenses influence which plant species herbivores consume, and how plant-herbivore interactions might influence plant community composition and diversity in the world's most species-rich forests. The interdisciplinary study will focus on the genetic, taxonomic, and functional diversity of the tree genus *Inga* (Fabaceae) and its insect herbivores at five sites in Central and South America (the Neotropics). *Inga* is the most locally diverse and abundant tree genus in Neotropical forests. This interdisciplinary study will measure plant defenses, including toxins, physical defenses and the attraction of ants (that may protect plants against herbivores) to sugar-producing nectaries on the leaves. DNA sequencing of herbivores and *Inga* will quantify diversity of species, test

whether closely related *Inga* have similar defenses, and determine whether herbivores choose hosts based on the similarity of their defenses.

It is hypothesized that if plants differ in their defenses, they will be attacked by different herbivores. If this is true then many plant species that differ in defenses can coexist as neighbors despite the fact that they are closely related. This process could help to explain the amazingly high local diversity of plants typical of tropical forests.

This research will be communicated to a variety of audiences to enhance appreciation of nature and science. The team will create a theater of biodiversity for school children and families in Utah, conduct Saturday science days for children from poor communities near the Brazil and Peru field stations, give presentations on tropical diversity for tourists at the Royal Botanic Garden, Edinburgh (UK), and develop the use of *Inga* in agroforestry. Agroforestry refers to the use of trees in plantations of coffee and cacao, for shade and to improve the habitat for wildlife, as well as to reforest, provide firewood, and improve soils in degraded areas. The integrative project will also create an open web-accessible site of results to share data and facilitate research by other scientists.

Right: Inflorescences of *Inga punctata* (Peru: Los Amigos)

Center right: Herbivores prefer tender, expanding leaves, such as these (*I. suberosa*; Brazil: Manaus, Reserva Ducke)



Tom Kursar, University of Utah



T. Kursar



T. Kursar



T. Kursar



T. Kursar

Above far right: An unidentified caterpillar in the family Lycaenidae consuming *I. cylindrica* (French Guiana: Nouragues)

Far left: An unidentified caterpillar (‘‘bagworm’’) consuming *I. bourgonii* (French Guiana: Nouragues)

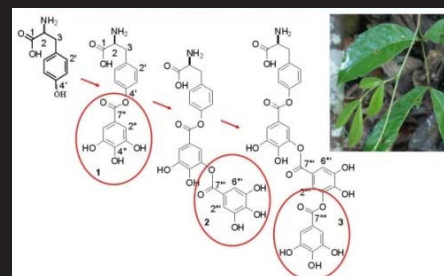
Near left: An unidentified caterpillar consuming *I. marginata* (French Guiana: Nouragues)



T. Kursar

Left: Ants are attracted to sugary rewards provided by the nectaries of expanding leaves. Nectar provides carbohydrates, but no protein. Therefore, ants also search for and consume high-protein herbivores, defending the plant in the process.

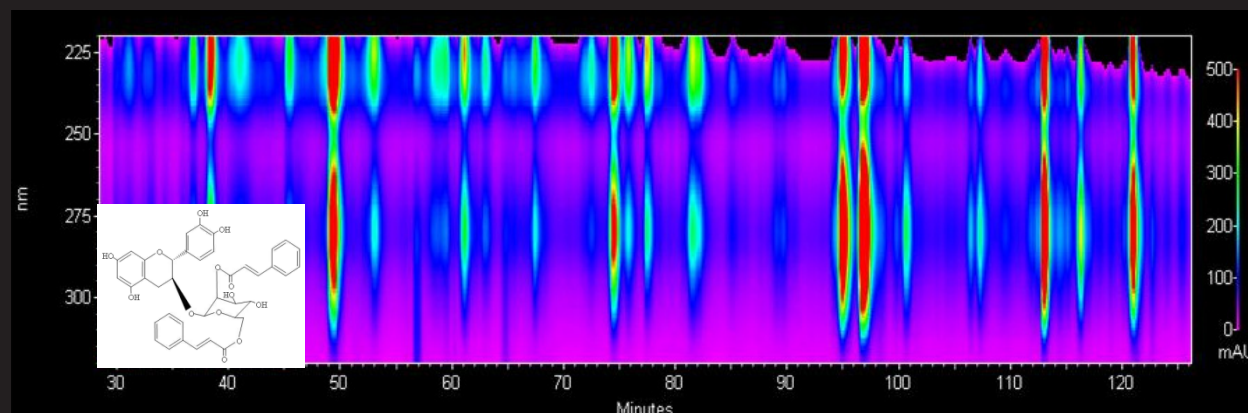
Right: The evolution of toxins in *Inga* begins by over-expression of the amino acid, tyrosine (leftmost compound). High concentrations of tyrosine are toxic to herbivores. Tyrosine derivatives, e.g. tyrosine depsides (circles 1–3), are found in other *Inga* species (Inset: *I. laurina*; Panama: Barro Colorado Island).



John Lokvam, University of Utah

Below: Separation of the series using chromatography on a column. Vertical axis shows detection of the toxins by ultraviolet light absorbance. Horizontal axis shows release time from the column for each toxin. The figure indicates approx. seven abundant compounds (red/blue) and 15 less abundant compounds (blue/blue-yellow).

Inset: One example of the structure of an extensive series of newly discovered chemical toxins made by *Inga umbellifera* (flavan-3-ols; Barro Colorado Island, Panama).



J. Lokvam

Lake Baikal responses to global change: The role of genetic, functional and taxonomic diversity in the plankton

Elena G. Litchman and Christopher A. Klausmeier, Michigan State University (NSF 1136710); Stephanie E. Hampton, University of California, Santa Barbara (NSF 1136637); Marianne Moore, Wellesley College (NSF 1136657); Edward C. Theriot, University of Texas, Austin (NSF 1136667); Lev Yampolsky, East Tennessee State University (NSF 1136706)

Microscopic plant- and animal-like plankton are the first links in aquatic food chains. This project will study the planktonic food web of the world's largest, oldest, and most biologically diverse lake -Lake Baikal in Siberia -to predict how native vs. non-native plankton will respond to accelerating environmental change in this system.

Human-induced global change is altering most ecosystems on Earth. How ecosystems will respond greatly depends on their biodiversity: genetic diversity may allow populations to adapt to change and functional diversity allows different species to carry out many different 'jobs' in the ecosystem, increasing its resilience. The exact mechanisms of how different dimensions of biodiversity determine ecosystem responses to global change are, however, poorly understood. An interdisciplinary team of researchers will use 60 years of unique ecological data, extensive field sampling, genetic analyses, laboratory experiments and novel mathematical models to examine for the first time multiple aspects of biodiversity in the largest, oldest and most biodiverse lake in the world – Lake Baikal in Siberia – and to predict how this ecosystem will respond to accelerating environmental change. Lake Baikal's planktonic food web (microscopic algae and zooplankton) fuels the rest of Baikal's incredibly diverse biota and is dominated by endemic species that are extremely sensitive to rising temperatures and other anthropogenic stressors. The researchers will determine if the genetic and functional diversity in the endemic species will allow them to adapt and persist in the changing climate or whether the lake's unique food web will collapse and be replaced by widely distributed (cosmopolitan) species, which may have dramatic consequences for the entire ecosystem, including the world's only freshwater seal.

Holding 20% of world's unfrozen fresh water, this UNESCO World Heritage Site is recognized internationally as a globally important freshwater resource, a treasure trove of biodiversity and a unique natural laboratory to study evolution. With an unprecedented diversity of endemic species found nowhere else, Lake Baikal serves as a model for ecosystems with highly unique biota and cold aquatic environments undergoing rapid warming.

Data collected on this project will be publically available so that their uses and value extend beyond this project and the researchers' laboratories. Researchers and students will engage in an interdisciplinary international collaborative research program. Funding will support graduate training in both applied and basic areas of science, including molecular biology, ecology, and informatics. The results will be communicated to environmental organizations in Russia and the US and to a US-based film team planning an IMAX movie about Lake Baikal and freshwater conservation. School teachers from Michigan, Texas and Tennessee will participate in the project and, together with researchers, develop educational activities on aquatic ecology, biological diversity and global change.



Nick Rodenhouse, Wellesley College

Above: Irkutsk State University Research Vessel Kozhov



N. Rodenhouse

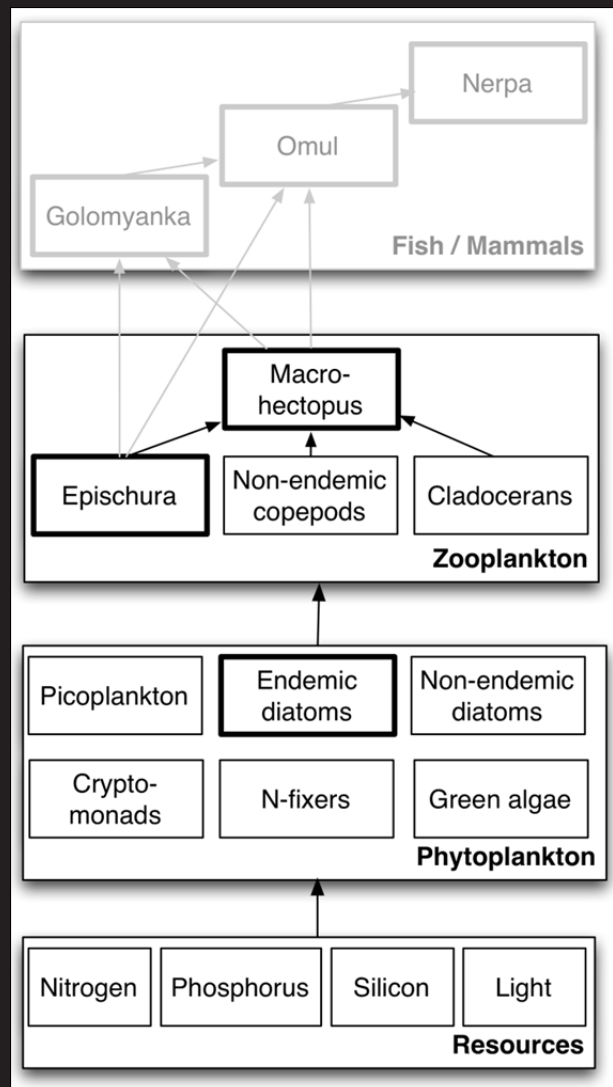
Above: Wellesley College students sampling Lake Baikal



Marianne Moore, Wellesley College

Above: Night sampling for golomyanka (*Comephorus* sp), an endemic oil fish

Right: Model food web of Lake Baikal: lower black boxes are modeled, gray boxes are non-modeled higher trophic levels. Thick borders denote endemic species that make up the backbone of the present-day food web.



Elena Litchman, Michigan State University

Integrating dimensions of Solanum biodiversity: Leveraging comparative and experimental transcriptomics to understand functional responses to environmental change

Leonie C. Moyle, David C. Haak, and Matthew W. Hahn, Indiana University (NSF 1136707)

This research highlights the role of environmental variation and herbivore defense in the remarkable diversity of wild tomato species by integrating analyses of DNA, gene expression, and phenotypes in this clade with data on their ecological and evolutionary history.

Global environmental change is expected to fundamentally alter patterns of biodiversity, but predicting the direction and magnitude of this change is extremely difficult. One factor in long-term responses to environmental change is the genetic basis of traits that mediate organism-environment interactions. The relative complexity of these traits and their interactions can influence how rapidly adaptation can occur and which traits are most responsive to environmental change. This research aims to understand how current biodiversity is shaped by environmental variation, by focusing on two critical plant traits: leaf eco-physiology (which influences plant responses to water, light, and carbon dioxide), and constitutive and induced defense responses (which influence plant responses to herbivores). Understanding the molecular genetics and adaptive history of these key traits will allow assessment of the mechanisms that may regulate future adaptive responses to environmental change.

This research will generate data on biodiversity in DNA sequences, in gene expression in response to abiotic and biotic stress, and in morphological and physiological traits, in 18 diverse ecotypes from 12 species in the plant group *Solanum* section *Lycopersicum* ('wild tomatoes'). This closely related group of Andean species spans a broad range of natural phenotypic and ecological variation, including ecotypes adapted to extremes in drought, salt, altitude, and temperature. Species also differ widely in the kind and magnitude of their defense responses to natural predators. As such, this group

is a potentially powerful model in which to understand the genetics of natural adaptive responses to environmental change over recent ecological and evolutionary timescales.

First, by coupling data on molecular genetic differences with differences in phenotypes and ecological interactions across the wild tomatoes (comparative transcriptomics), the project will identify the genetic changes that have attended adaptive differentiation. Second, examining gene expression responses in different ecotypes to drought and induced defense (experimental transcriptomics) will clarify how molecular responses to these abiotic and biotic stresses are integrated, and whether this changes over short ecological and evolutionary timescales. Finally, combining these findings with existing data, the research will generate a core set of loci underpinning functional responses to abiotic and biotic environmental variation across an entire group of wild species.

The project will contribute to workforce by training researchers in a broad set of skills at the interface of experimental genetics, genomics and bioinformatics. By examining wild relatives of several important crops, including tomato, potato, and pepper, this research may also help identify valuable natural variation that confers plant tolerance to critical environmental stresses. Finally, uncovering the genetics of diversification is crucial in the Andes, where land-use and climate change threaten a cradle of biodiversity with an estimated 12% of global flowering plant diversity.

Right: Diversity of leaf shapes and sizes among wild tomatoes, *Solanum* spp

Top row: *S. peruvianum*, *S. galapagense*, *S. chessemaniae*, *S. pennellii*, *S. habrochaetes*

Middle row: *S. pimpinellifolium*, *S. lycopersicoides*

Bottom row: *S. neorickii*, *S. chilense*, *S. lycopersicum* var. *cerasiforme*, *S. ochranthum*.



Leonie Moyle, Indiana University



David Haak, Indiana University



D. Haak

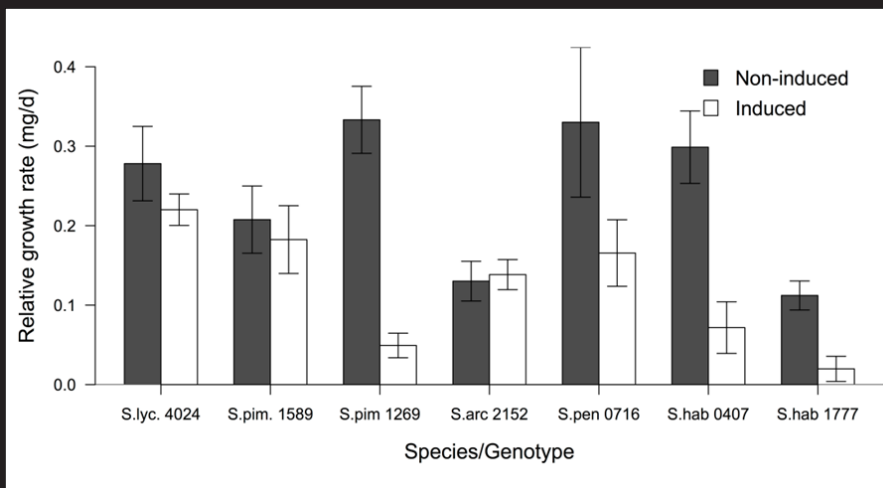


D. Haak

Above left: A tobacco hornworm (larvae of the Carolina sphinx moth, *Manduca sexta*) navigates the dense hairs on leaves and buds of *S. habrochaetes*

Above center: Silhouette of *M. sexta* feeding on a leaf of *S. pennellii*

Above right: *M. sexta* tastes and rejects a leaf of *S. pimpinellifolium*



Left: Natural *Solanum* variation in non- and induced defense to the specialist herbivore *M. sexta*

X-axis: seven genotypes that span within and among species diversity Y-axis: shows growth rate of *M. sexta* larvae on each genotype. Induction via Jasmonic acid-treatment

D.Haak

Functional diversity of microbial trophic guilds defined using stable isotope ratios of proteins

Ann Pearson and Peter Girguis, Harvard University (NSF 1136484); Jennifer Macalady, Pennsylvania State University, University Park (NSF 1136218)

Studying the ecological interactions among microbes is difficult given their immense diversity and the scale of observation. This project will use isotopic ratios of carbon, nitrogen, hydrogen, and sulfur produced during microbial metabolism to link guilds of microbes to their roles in biogeochemical and ecosystem processes. This novel approach will contribute to our understanding of what maintains functional and genetic diversity in microbes and, by extension, the roles those microbes play in ecosystems.

Recent advances in DNA sequencing technology have accelerated the pace of discovery of species and gene distributions. This contrasts with slower progress in linking environmental genetics and taxonomic diversity to the functions, resource utilization, and ecological niches occupied by species. This work will develop a novel application of isotope geochemistry and will apply it in the field of aquatic biochemistry as a first step toward tackling these challenges. The goal of the project is to combine natural isotope ratio data with proteomics. Different metabolic processes yield different ratios of the stable isotopes of carbon, nitrogen, hydrogen, and sulfur. By measuring these ratios on specific proteins with simultaneous sequencing, these natural isotope signals can attribute biogeochemical processes (functions) to specific microbes (taxonomic and genetic information). The approach will be called P-SIF (protein stable isotope fingerprinting). Because this is a novel methodology, the project first will seek to identify the fundamental principles of natural isotopic sorting that could result from different types of trophic ecosystem structure. This will be implemented using pure cultures and then tested on a model ecosystem from a stratified lake. Example questions include: How does the distribution of P-SIF fingerprints in a mixed community scale with the genetic diversity of a sample's metagenome and expression of its metaproteome? Does higher diversity predict more trophic levels?

Examining this “how, when, and why” of microbial processes yields insight about environmental conditions on Earth today, in the past, and about potential human impacts on our future. This project will help to develop a concept of trophic guilds and ecosystem dependence for microbes. Such concepts are well developed in macro-ecology, but remain less well understood for microbial diversity. Ecosystem maintenance and conservation is not possible without a better understanding of what maintains microbial functional and genetic diversity. The success of this project could lead to many further applications to understanding the physiological and/or ecological roles of uncultured microbes in the environment. The project has three principal investigators: an isotope geochemist, a microbial physiologist, and a microbial ecologist. This team is ideally suited to achieve the interdisciplinary goal of linking geochemistry with microbial ecology. The proposed activities will educate a post-doctoral investigator, two graduate students, and several undergraduate summer students. Additional activities such as The Cambridge Science Festival and Science by the Pint (<http://cambridgesciencefestival.org/Home.aspx>; <https://sitn.hms.harvard.edu/>), will communicate the research to the public.



Left: Mahoney Lake, (Canada: British Columbia, Penticton)

Jennifer Glass, Arizona State University

Right: Direct sample of the Mahoney chemocline, showing a dense community rich in photosynthetic and chemosynthetic sulfur bacteria



J.Glass



Left: Hotel room “kitchen laboratory” (Canada: British Columbia, Penticton)

J.Glass

The climate cascade: Functional and evolutionary consequences of climatic change on species, trait, and genetic diversity in a temperate ant community

Nathan J. Sanders, University of Tennessee, Knoxville (NSF 1136703); Robert P. Dunn, North Carolina State University (NSF 1136717); Aaron M. Ellison, Harvard University (NSF 1136646); Nicholas J. Gotelli, Bryan A. Ballif, and Sara I. Cahan, University of Vermont and State Agricultural College (NSF 1136644)

Sanders and colleagues will study adaptations to climate change in a common foraging ant in eastern US forests to understand the mechanisms that allow some species to adapt to shifts in climate rather than migrating or going extinct.

Climate is rapidly changing and biodiversity is changing with it: species evolve or disappear locally, regionally, or entirely. However, we know surprisingly little about the mechanisms that lead to these shifts in biodiversity. Why do some species track changes in environmental temperatures while others stay put? What physiological and evolutionary mechanisms allow species to stay put?

This project builds off of an ongoing warming experiment carried out by a team of investigators located at four institutions (University of Tennessee, North Carolina State University, University of Vermont, and Harvard Forest). The core of the research focuses on how populations and species of forest ants adapt to climate change and avoid local extinction. Why ants in forests? Ants process soil, cycle nutrients, and disperse seeds of perhaps more than 50% of “spring ephemerals” – understory herbs such as trillium, bloodroot, and winged polygala – which flower on the forest floor in early spring before tree canopies close. Ants also respond, often quickly, to changes in air temperature, so climate change could have dramatic implications for the structure and function of eastern US forests.

Samples of the most common ant species will be collected from forests throughout the eastern US, and gene sequencing will be used to reconstruct the evolutionary history of these ants to reveal genes that may have evolved in response to past climate change. Genes will also be sequenced

from ants collected from the ongoing experimental warming chambers at Harvard Forest and Duke Forest that have been continuously heated (from ambient temperatures up to +5 °C) for the past three years. In controlled laboratory experiments, ants will be briefly exposed to a range of high temperatures predicted by climate change models, and the production of heat shock proteins will be measured. Heat-shock proteins are molecules that are produced in greater quantities when organisms are exposed to high temperatures, and they represent important adaptations to heat stress. Heat shock proteins from different ant species will be analyzed to determine their biochemical structure, which can provide clues to how well species can adapt physiologically to high temperatures. Taken together, the results of this research will help to understand the many ways that key species are likely to respond to climate change. Additionally, it will provide information about the interplay among evolutionary history, behavior, and ecological interactions in response to climate change.

This research will train undergraduate and graduate students, and provide public outreach and education on the effects of climate change on biodiversity. Summer high school outreach programs for both teachers and students will be enhanced, and citizen-scientists will be engaged in documenting the effects of climate change on biodiversity.



Aaron M. Ellison



A.M. Ellison



A.M. Ellison

Above left: A member of the *Aphaenogaster rudis* complex tending a brood of larvae and pupae

Above right: Species in the *A. rudis* complex nest in and around damp, fungus-laden soil

Left: This photograph shows a 22 m³ atmospheric warming chamber *in situ* at Harvard Forest



Paul J. Hanson

Below: The Climate Cascade team: PI N. Sanders (far left), co-PIs A. Ellison (far right), R. Dunn (back row, right of Sanders), N. Gotelli (center, with black vest), with graduate students and post-docs from the University of Tennessee, Harvard University, North Carolina State University, and the University of Vermont



A.M. Ellison

An integrated study of energy metabolism, carbon fixation, and colonization mechanisms in chemosynthetic microbial communities at deep-sea vents

Stefan M. Sievert, Jeffrey S. Seewald, Craig D. Taylor, Woods Hole Oceanographic Inst (NSF 1136727); Dionysios I. Foustoukos, Carnegie Institution of Washington (NSF 1136608); Ramunas Stepanauskas, Bigelow Laboratory for Ocean Sciences (NSF 1136488); Costantino Vetriani, Rutgers University, New Brunswick (NSF 1136451)

This project will establish an interdisciplinary, international research program to better understand the microbiology and biogeochemistry in deep-sea hydrothermal vent ecosystems.

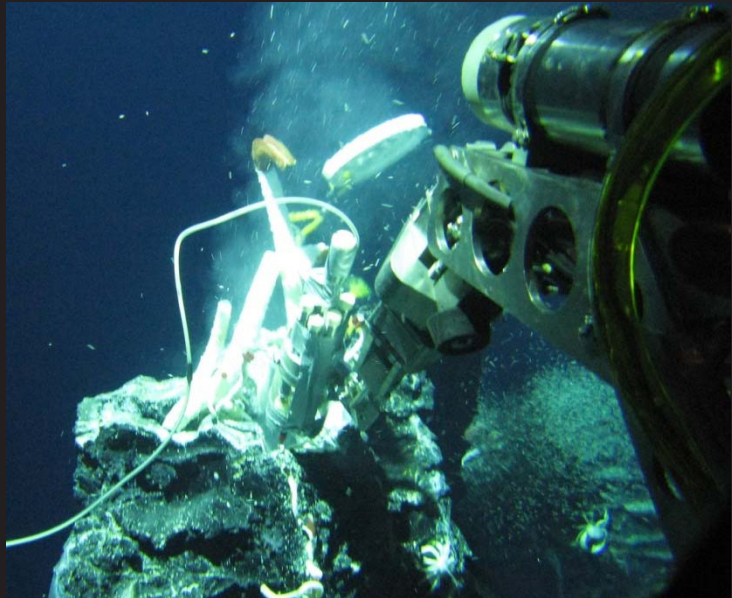
First discovered in 1977, deep-sea hydrothermal vents, are 'poster child' ecosystems where chemosynthesis rather than photosynthesis, is the primary source of organic carbon, fueling complex and productive ecosystems. Chemosynthesis is the production of organic matter from CO₂ coupled to inorganic chemical reactions to obtain energy. While biological productivity at vents is generally well-described, significant gaps remain in our understanding of the microbiology and biogeochemistry of these fascinating ecosystems. In particular, we do not have a good understanding of the metabolic pathways used by the microbes, the rates of the catalyzed reactions, the specific microorganisms mediating these reactions, the amounts of organic carbon being produced, and the larger role of these ecosystems in global biogeochemical cycles.

To fill these gaps and better understand the fluxes of energy and matter at deep-sea vents the researchers will pursue an *interdisciplinary, international* program. This project will couple an assessment of taxonomic diversity using cultivation-dependent and - independent approaches with methodologies that address genetic diversity, including a) metagenomics (genetic potential and community diversity), b) single cell genomics (genetic potential and diversity of uncultured single cells), c) meta- transcriptomics and -proteomics (identification and function of active community members; realized potential of the community). To

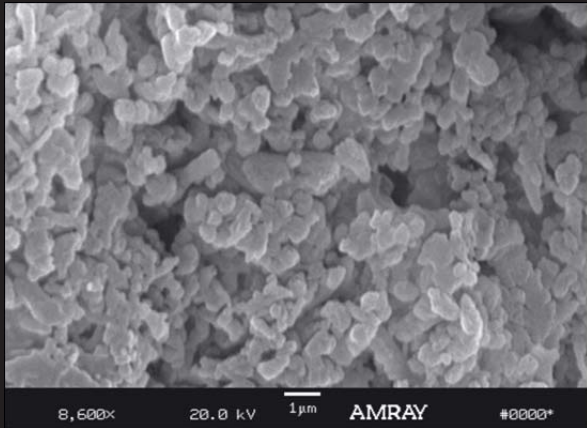
assess function and response to the environment, these approaches will be combined with 1) *in situ* rate measurement of chemoautotrophic production, 2) geochemical characterization of microbial habitats, and 3) shipboard incubations under simulated *in situ* conditions (hypothesis testing under controlled physicochemical conditions). Network approaches and mathematical simulation will further be used to reconstruct the metabolic network of the natural communities. The integration of laboratory and field experiments in combination with a suite of cutting edge analytical techniques will create unprecedented opportunities that will lead to unique insights into the functioning and environmental interactions of deep-sea vent microbial communities, ultimately enabling us to place these systems into a quantitative framework and thus a global context.

This is an interdisciplinary and collaborative effort between 4 US and 4 foreign institutions, creating unique opportunities for networking that benefit also the involved students and postdoctoral associate. A variety of educational and public outreach activities aiming at a diverse audience ranging from grades 4 – 12, community colleges, and undergraduate universities to the general public are an integral part of this project. The research cruise will also be featured on the highly successful WHOI Dive & Discover program.

Right: At “Crab Spa,” a diffuse-flow hydrothermal vent site (East Pacific Rise at 9°N 50', 104°W 17'), the manipulator arm of the submersible *Alvin* holds a sensor developed by collaborator Nadine Le Bris, that measures temperature, pH and sulfide *in situ*. Chemosynthetic microbial communities manifest themselves as white biofilms attached to the basalt, are released from the sub-seafloor and suspended in the fluid or live in symbioses with invertebrates such as the giant tube-worm *Riftia pachyptila* (left of center). An integration of *in situ* and laboratory-based studies to assess the function and diversity of these microbial communities is at the core of this project.



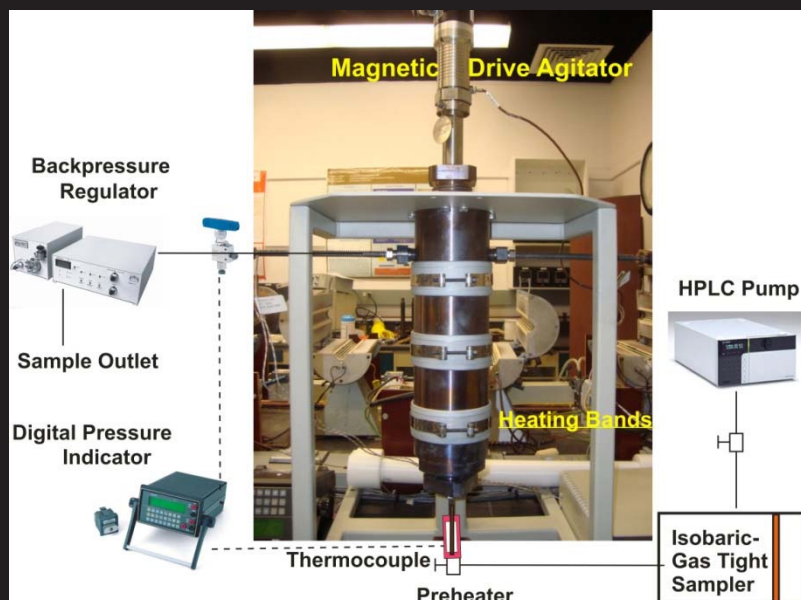
Stefan Sievert, Woods Hole Oceanographic Inst



Costantino Vetriani, Rutgers University

Left: Scanning electron micrograph of chemosynthetic biofilm collected from a deep-sea hydrothermal vent

Right: Dual-flow titanium reactor to investigate metabolic rates and growth efficiency of chemo-autotrophs across redox gradients. This experimental setup facilitates continuous culturing experiments to be performed in laboratory under seafloor temperature and pressure conditions.



Dionysis I. Foustoukos, Carnegie Inst. of Washington

Functional diversity of marine eukaryotic phytoplankton and their contributions to C and N cycling

Bess B. Ward and Daniel M. Sigman, Princeton University (NSF 1136345); Andrew E. Allen, J. Craig Venter Institute, Inc. (NSF 1136477)

This project will use two North Atlantic sites in two seasons to link genetic diversity and species composition of phytoplankton communities to the biogeochemistry of the surface ocean.

Phytoplankton form the basis of the marine food web and thus are a crucial element in the biological pump whereby atmospheric CO₂ is sequestered in the deep ocean. For decades, biological oceanography focused on eukaryotic phytoplankton. In the 1970-80's, it was found that single celled picocyanobacteria are numerically dominant in oceans and responsible for a large fraction of ocean photosynthesis. What resulted was a new paradigm in which the picocyanobacteria dominate upper ocean biology and biogeochemistry. In fact, new data support the classic view that the eukaryotic phytoplankton are disproportionately important in both N and C cycling, even in regions where very small cells dominate and where the eukaryotes themselves are in the "pico" size fraction. In oligotrophic environments, where very small cells dominate, *in situ* recycling appears to supply most of the nitrogen (i.e., ammonium) required for primary production. On the basis of still quite limited molecular surveys, it is recognized that the diversity of both large and small eukaryotic phytoplankton is greater than previously thought and that the most abundant and widespread eukaryotes are probably not in culture and may not be closely related to known cultivated organisms.

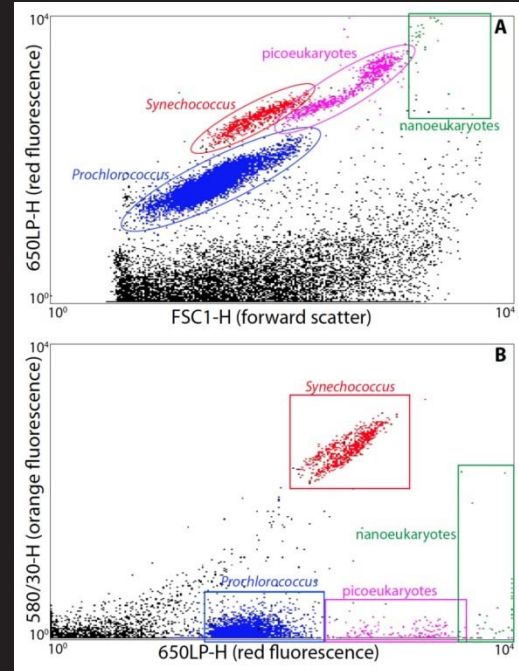
Ward and colleagues will investigate the taxonomic, genetic and functional diversity of eukaryotic phytoplankton and link this diversity and assemblage

composition to the carbon and nitrogen biogeochemistry of the surface ocean at two North Atlantic sites (subarctic and subtropical) in two seasons. They are investigating taxonomic diversity by identifying the components of phytoplankton assemblages using molecular, chemical and microscope methods. Genetic diversity will be explored at several levels, including direct sequencing of clone libraries of key functional genes and metatranscriptomic sequencing and microarray analysis of size fractionated/sorted phytoplankton assemblages. Finally, genetic and taxonomic diversity will be linked to functional diversity in C and N assimilation in size-fractionated and taxon-sorted populations using natural abundance and tracer stable isotope methods.

This project will contribute to fundamental research and education through development of methods of isotope analysis in environmental samples; undergraduate teaching and research experiences; and training the next generation of microbial ecology/biogeochemistry researchers through classroom and research experiences at the graduate level. In addition, the researchers will provide a new module, *The Forests and Deserts of the Ocean*, to the Princeton outreach program for middle school teachers (QUEST, Questioning Underlies Effective Science Teaching).



Sarah Fawcett, Princeton University

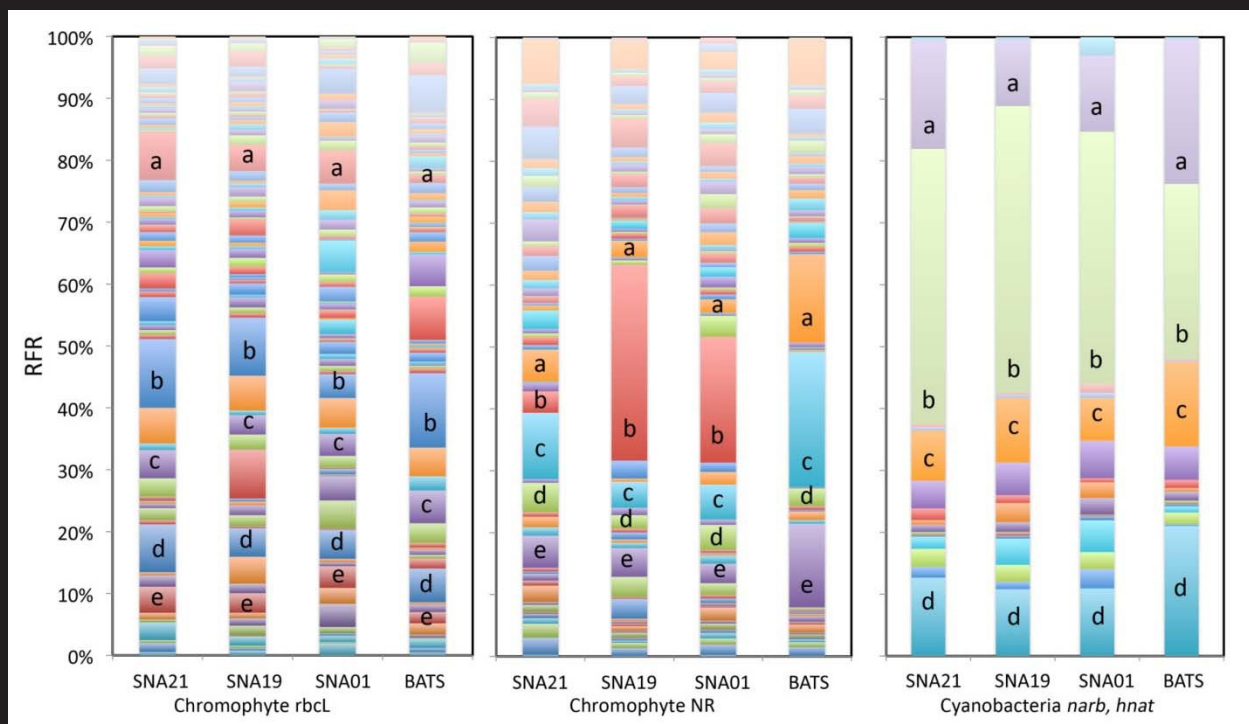


S. Fawcett

Above left: Post-doc Katye Altieri and graduate student Sarah Fawcett deploying a CTD rosette (used to measure sea water conductivity, temperature and density) for the Bermuda Atlantic Time-series Study (BATS)

Above right: Scattergram of flow cytometry data showing differentiation between different groups of phytoplankton on the basis of size and autofluorescence

Below: Relative contribution of diverse archetypes to the phytoplankton community in the Subarctic North Atlantic (SNA; May 2009) and at BATS (March 2009) analyzed on Phytoarray-2. The colors represent Relative Fluorescence Ratio, the fraction of total fluorescence due to each probe (average of two replicate arrays for each sample)



Bess Ward, Princeton University

INTERNATIONAL RESEARCH COORDINATION NETWORK: A research coordination network for biodiversity of ciliates

PI: John Clamp, North Carolina Central University (NSF 1136580)

US MEMBERS: John Clamp; Laura Katz, Smith College; Chris Lobban, University of Guam; Micah Dunthorn, University of Kaiserslautern, Germany

CHINA MEMBERS: Weibo Song, Ocean University of China, Qingdao; Xiaofeng Lin, South China Normal University, Guangzhou.

OTHER COUNTRIES: Alan Warren, Natural History Museum, London, United Kingdom; Laura Utz, Pontificia Universidade Católica do Rio Grande do Sul, Brazil

This project, jointly supported by the National Natural Science Foundation of China, will establish an International Research Coordination Network for Biodiversity of Ciliates. The network will include researchers from the US, China, the UK, and Brazil and will broaden exploration of these important protists.

Ciliates are a major group of unicellular, eukaryotic organisms that play important roles in nearly all ecosystems and serve as model organisms for basic research in genetics and cell function. Approximately 7,500 species are known, but three times that many may be undiscovered, especially in poorly explored places like tropical forests or the deep ocean.

Better knowledge of the biodiversity of ciliates could translate into more effective management of ecosystems or new model research organisms, but achieving these objectives has been slower and more difficult than with multicellular organisms. Modern studies of biodiversity often rely on DNA from preserved specimens in museums, but there is no such archive for ciliates. Also, sequencing most genes of ciliates is more challenging than in animals or plants. Lastly, researchers who study biodiversity of ciliates are scattered thinly and unevenly across the world, and many are younger investigators who have little money for travel to professional meetings or other laboratories to build collaborations, which are the best way to make rapid progress.

The Research Coordination Network for Biodiversity of Ciliates (RCN-BC) is a project begun by Chinese and US laboratories that will address these prob-

lems. It will be a worldwide network of researchers designed to lower the barriers to research on ciliate biodiversity, an 'engine' for generating new collaborations, new procedures for archiving material, and – most significantly – new research projects that unite the three dimensions of biodiversity. The RCN-BC will create the means to advance research in biodiversity of ciliates more quickly by (1) sponsoring workshops and symposia to build strategies and develop techniques; (2) creating archives for preserved samples of cells and DNA; (3) maintaining a website to report activities, attract new members, promote collaborations, and share data; and (4) funding travel for researchers.

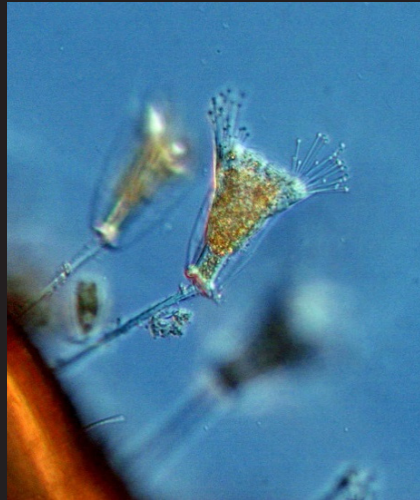
The RCN-BC will be a model for accelerating multidimensional investigation of biodiversity in other protistan groups. Also, students at Minority Serving Institutions (MSIs) traditionally get scant exposure to areas of biology outside biomedicine. The RCN-BC will create an email listserv of contacts at MSIs to inform faculty and students about the RCN-BC, especially connections between biodiversity and biomedicine. Students from underrepresented minority groups (African-American, Pacific Islander) will be included in two workshops.



Examples of two of the many species of ciliated protists that occur in environments world-wide:

Left: *Diophrys* sp., a hypotrich; these ciliates form one of the largest groups in the phylum and are significant components of food webs in marine, freshwater, ephemeral, and terrestrial habitats.

Right: *Acineta tuberosa*, a suctorian; these ciliates attach to many sorts of substrates, including a wide array of animals, and prey on other ciliates.



Left: Distribution of members in the Research Coordination Network for Biodiversity of Ciliates. The RCN has grown out of active research collaborations between the Laboratory of Protozoology at the Ocean University of China and other major laboratories (steering committee members are labeled)

Below: Students and faculty of the Laboratory of Protozoology, Ocean University of China, Qingdao (Spring 2007).

Dr. W. Song, principal Chinese RCN partner (fourth from right in standing row); Dr. A. Warren, Museum of Natural History, UK, is a long-time Qingdao lab collaborator (left of Dr. Song); Dr. J. Clamp, N.C. Central University, is the principal US RCN partner, project PI, and long-time collaborator with Dr. Song and others in the Qingdao lab.



The microbial basis of animal speciation

Seth Bordenstein, Vanderbilt University (NSF 1046149)

This project will investigate the role host-associated microbial communities play in structuring species complexes and diversification in a genus of parasitoid wasps.

One of the central questions in biology is how do new species arise- that is, how does one species become two and so on to ultimately produce the more than 1.8 million species that now inhabit the planet. Traditionally, animal species are categorized as groups of individuals that can interbreed, and new species thus arise by the accumulation of genetic mutations that ultimately cause the inability for two populations to interbreed. Once these barriers to interbreeding evolve, speciation is underway.

However, animal species may also change by acquiring differences in the millions of bacteria that typically inhabit them in symbiotic relationships. For instance, in humans 90% of the cells in the body are microorganisms, not human cells. This research will address a major gap in our knowledge about how biodiversity arises in animals: whether or not the symbiotic community of bacteria within a host can contribute to hybrid lethality between host species. The investigation has three aims using several species of interfertile parasitoid wasps in the genus *Nasonia* that vary in their level of hybrid lethality. First, the investigators will test if the normal, resident bacteria within a species are different than those in hybrids. Alterations of the microbial community in hybrids would suggest an incompetence of the host to regulate a normal consortium of bacteria. Second, they will test the prediction that the host's genes that are used to regulate its immune system and defend against pathogens are not turned on properly in hybrids, and these changes in hybrid genes will be associated with changes in the hybrid's bacterial community. Third and finally, the researchers will test if hybrid mortality between

the species is due to either a reduction in beneficial bacteria or an increase in pathogenic bacteria. To do this they will investigate whether hybrids free of their bacteria or transplanted with specific infections die prematurely or not.

The studies will integrate genetic, taxonomic, and functional dimensions of animal-microbe symbioses to comprehensively determine the consequences of bacterial symbionts on speciation in a model system. The research will characterize new species of bacteria and existing species of bacteria in novel functions. Genetic aspects of the studies will include the effects that hybridization can have on animal gene expression and the genetic diversity of their bacterial symbionts. Functionally, this work will unravel the host's dependence on bacterial symbionts throughout development and test if bacterial symbionts are as important as genes in the generation of new animal species.

Broader impacts of this project include the development of a new course at Vanderbilt University that will involve undergraduates in the research, creation of an online repository for taxonomic information on the symbionts discovered in this research, dissemination of data through publically accessible databases, and extensions to understanding speciation and symbiosis in new ways across all animals, including humans. Finally, the proposed research will provide training to one graduate student, one research assistant, and several undergraduates involved in volunteerships, internships, and research for credit.

Brucker, RM & SR Bordenstein. 2011. The roles of host evolutionary relationships (Genus *Nasonia*) and development in structuring microbial communities. *Evolution*. DOI: 10.1111/j.1558-5646.2011.01454.x



Left: A *Nasonia* parasitoid wasp, model organism of this Dimensions of Biodiversity project. *Nasonia* are smaller than fruit flies and parasitize house flies or blow flies.

Right: A *Nasonia* female uses her ovipositor to pierce the fly host casing and deposit her eggs inside. The wasp offspring develop in this protective environment.

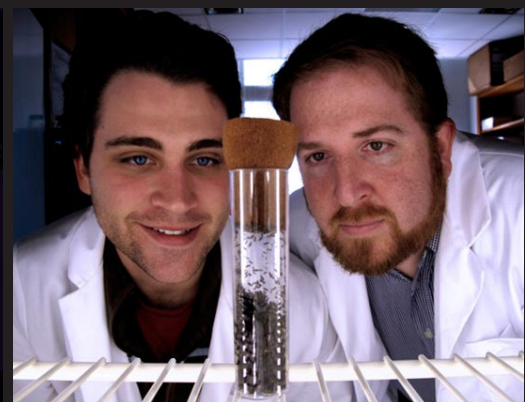
Below: The four species of the genus *Nasonia* are interfertile, but hybrids display varying levels of lethality during the larval-pupal transition. These three images demonstrate the reduced success of hybrid larvae.



Left: A conceptual framework showing that the general microbiota (bacterial colonies represented on the culture plate by different colors) may diverge in parallel with the host's evolutionary relationships. The trunk and three branches of the tree depict the relationships of both the bacterial symbiont communities and the host's genes.

Below Left: The head of *Nasonia* wasp that was captured in detail by a scanning electron microscope. The image is false colored purple.

Below Right: Seth Bordenstein, right, and Robert Brucker examining a bottle filled with *Nasonia* wasps.



All images: Robert Brucker & Seth Bordenstein, Vanderbilt University

Deconstructing diversity and ecosystem function at multiple spatial & genetic scales in a keystone plant-microbe symbiosis

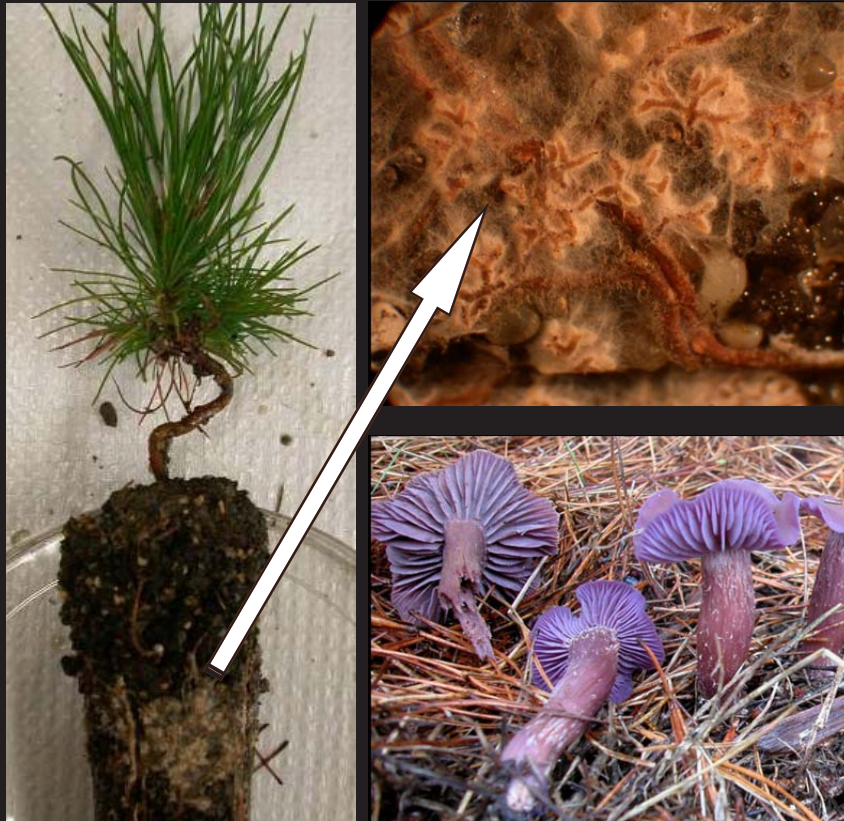
Thomas Bruns and John W. Taylor, University of California, Berkeley (NSF 1046115); Kabir G. Peay, University of Minnesota – Twin Cities (NSF 1045658); Rytas Vilgalys, Duke University (NSF 1046052)

This project will consider soil fungal communities associated with pine-dominated forests in North America, which are poorly known and may serve as a model system for understanding microbial community dynamics.

Fungi are a critical component of the biodiversity and functioning of terrestrial ecosystems. They play many roles in the environment – fungi are the primary degraders of dead plant material, they are major pathogens of living plants and soil animals, and they also form mutually beneficial symbioses with the roots of most plant species. Like other groups of cryptic, soil dwelling organisms, fungal communities are hyper-diverse and poorly known in even the best-studied ecosystems. Major advances in molecular biology techniques, such as Next Generation high-throughput DNA sequencing, are just beginning to allow robust exploration of taxonomic diversity in soil communities. However, simple enumeration of species diversity reveals little about the ecological processes structuring communities, or how community structure affects key ecosystem processes. This research project will provide the first continental-scale sample linking taxonomic, genetic and functional diversity of a key guild of plant root symbionts – the ectomycorrhizal fungi – from pine ecosystems across North America. Ectomycorrhizal fungi form symbiotic relationships with the roots

of dominant forest plants and provide them with nutrients and water in exchange for photosynthetically-fixed carbon. Despite the importance of ectomycorrhizal fungi in global nutrient cycles, little is known about large-scale patterns of fungal community structure relative to plants, animals, or even bacteria. This project will establish patterns of gene flow and adaptation for multiple ectomycorrhizal fungi across North America and measure variation in key biochemical characteristics of individuals, populations and species.

The project will result in a large, open access database of taxonomic barcode and functional genes that can be used by researchers to generate predictive models of fungal ecosystems. It will include training of graduate students and post-doctoral scholars in cutting-edge techniques in an understudied field, will result in outreach activities targeted toward the general public, and will include activities for K-12 students and educators designed to foster early student interests in fungi.



Left: Mycorrhizal symbiosis is an integral component of forest ecosystems.

Far left: Most dominant tree species in temperate forests, such as pines, depend on fungi for the acquisition of soil nutrients necessary for their growth and reproduction

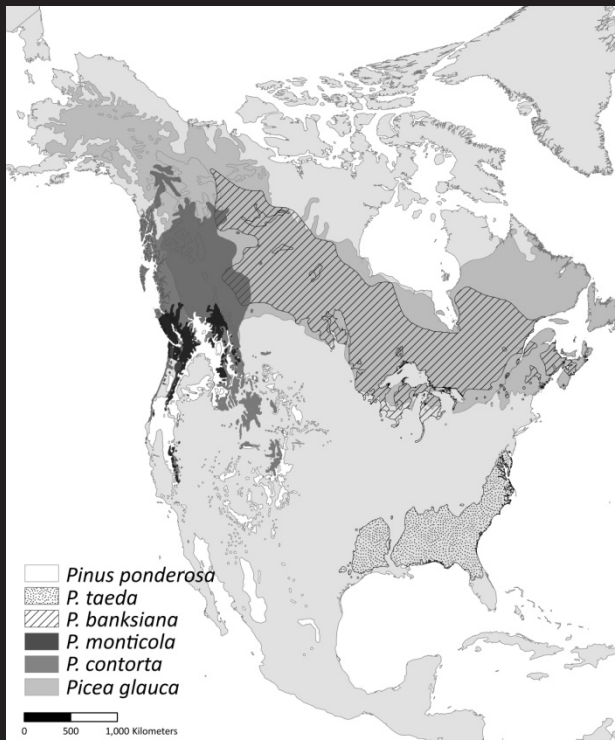
Left above: Plant and fungal tissue intermingle in roots to form a new absorptive organ – the mycorrhiza. In ecto- mycorrhizas, fungal tissue encases the plant roots and nutrients are absorbed by hyphal filaments that forage the soil

Left below: Many of the fungi involved in ectomycorrhizal symbiosis produce conspicuous fruiting bodies, commonly known as mushrooms

Kabir G. Peay

The diversity of these symbiotic fungi is poorly known, but may have important implications for ecosystem health.

Below: Sampling design for assessing spatial, historical & environmental drivers of ectomycorrhizal fungi (EMF) diversity across multiple spatial scales:



Thomas D. Bruns

Left: N. American distribution for selected host species

Below left: Potential regional arrangement of six plots for sampling of *Pinus taeda* EMF

Below right: Nested sampling design for each plot. Soil samples will be taken at the vertices of each rectangle (n=16 samples per plot). Six plots will be sampled for each host species for a total of 36 plots in the study.



T.D. Bruns

Can evolutionary history predict how changes in biodiversity impact the productivity of ecosystems?

Bradley Cardinale, University of Michigan Ann Arbor (NSF 1046121); Charles F. Delwiche, University of Maryland College Park (NSF 1046075); Todd H. Oakley, University of California Santa Barbara (NSF 1046307)

Cardinale and colleagues will examine how evolutionary processes among algae generate and maintain diversity at levels from genes to ecosystems in freshwater lakes.

Understanding how biodiversity loss will impact the productivity and sustainability of Earth's natural ecosystems is a primary goal of modern science. The goal of this project is to identify and predict which extinction events are likely to have the greatest impacts on *primary production*, the process by which plants capture sunlight and use atmospheric CO₂ to produce energy at the base of the food web. These researchers hypothesize that the impacts of species extinction on primary production can be predicted if one knows the evolutionary relationships among species. They propose that evolution has led to a functional 'division of labor' that determines how efficiently groups of plants capture essential resources like nutrients or light. If evolution leads to species that are genetically unique, and ecologically irreplaceable, then we should be able to use our understanding of evolution to predict which species losses will have the greatest impacts on processes like primary production. This project includes experts in genomics, phylogenetics, and ecology integrating research efforts to understand how one of the most widespread and ecologically important groups of algae controls lake productivity throughout North America. We will use molecular data to determine whether communities of algae that live together are more genetically diverse than one would expect by random chance, and then create experimental lakes of algae where the species differ in their evolutionary history, and therefore, their levels of genetic divergence.

This will allow them to directly measure how evolutionary and genetic differences control the functional differences among species and, in turn, how these functional differences influence primary production. Finally, they will identify genes that allow species to use biologically essential resources in different ways and determine which genes are turned 'on' and 'off' as species try to survive when in competition with each another.

This work will help prioritize conservation efforts by identifying species that have the largest impacts on important ecological processes. It will also provide an underpinning for conservation prioritization in ecosystems that are too large (rain forests), too remote (the ocean floor), or too endangered (threatened species) to perform biodiversity experiments. This project will include participation by a variety of students, ranging from high school interns, to Ph.D. students, to postdoctoral fellows. These individuals will be trained in an exciting new area of research that merges genetics and evolution to understand modern environmental problems. The project also will develop a new college-level course that integrates genomics, phylogenetics and ecology. This course will provide our next generation of researchers with the ability to address environmental problems with tools from the level of genes to whole ecosystems.

Cardinale, B.J. 2011. Biodiversity improves water quality through niche partitioning. *Nature* 472:86.

Cardinale, B. J., J.E. Duffy, A. Gonzalez, D.U. Hooper, C. Perrings, P. Venail, A. Narwani, G.M. Mace, D. Tilman, D.A. Wardle, A.P. Kinzig, G.C. Daily, M. Loreau, J.B. Grace, A. Larigauderie, D. Srivastava, and S. Naeem. 2012. Biodiversity loss and its impact on humanity. *Nature* 486:59.



The investigators will use three approaches to identify and predict which extinction events are likely to have the greatest impacts on primary production in lake communities: (1) an evolutionary approach that determines whether genes are phylogenetically conserved for natural species assemblages, (2) a genomic approach that determines whether conservation of genes translates to unique ecological niches among species, and (3) an ecological approach that determines whether niche differences impact the productivity of entire communities.

Functional, genetic, and taxonomic diversity of plant-fungal interactions along climatic gradients and their role in climate change driven species migrations

Richard Lankau, University of Georgia (NSF 1045977)

The largely unseen world of soil fungi is intimately linked to plant communities. This award will support research to understand how the taxonomic diversity of soil fungi interacts with the genetic diversity of two tree species.

Climates are currently warming at unprecedented rates. In order to avoid extinction, species must move to track the changing climate, or evolve to tolerate warmer conditions. Researchers have predicted that many eastern forest tree species will shift their ranges considerably as climates warm, by expanding to the north or up in elevation, and contracting from the south or down to lower elevations. Long-term data from the eastern US has already shown the beginning stages of this range movement for some species. However, these predictions are based on very simplified models that do not consider how interactions among species may constrain or promote a given tree species' ability to expand its range. Most plant species, especially forest trees, rely on intimate associations with microbial species living in soil in order to capture the resources they need for proper growth. Little is known about how these invisible, but very important, soil microbes are distributed across the continent, and how they will respond to climate change. This basic knowledge on the geographic distribution of these soil microbes will be important to predict how well tree species will be able to track their moving climates. For instance, if a tree species shifts north 100 kilometers to maintain its current climate conditions, will it be encountering a completely different soil microbial community? Or will some of its preferred microbial partners already be present in that new area? Additionally, there is currently very little known about the climatic

tolerances of important soil microbial groups. As climates warm, will they also shift their ranges? Or are they so broadly distributed already that the predicted rates of climate warming will exert little pressure on them?

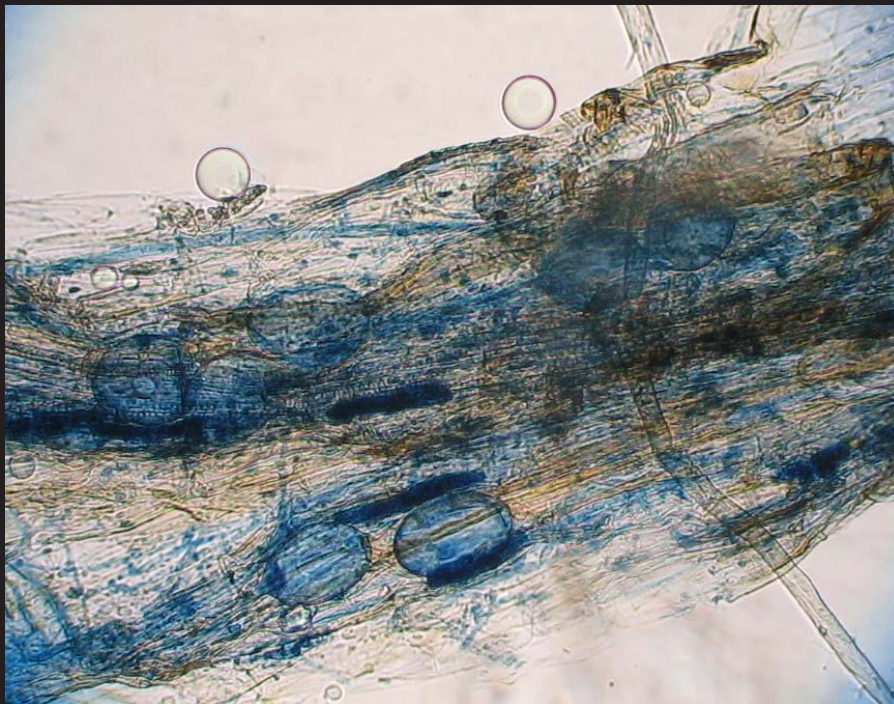
In this project soil microbial sampling will provide basic information on how these microbes are distributed as well as how their distribution relates to current climates and genetic structure of the tree species. Trees and soil microbes will likely not move at equal speeds as climates change. For instance, if these microbes are not able to disperse as quickly as their host tree species, then this may constrain the tree's ability to migrate north (as it will have to wait for its microbial associates to catch up). Therefore, experiments will test the functional consequences for tree growth for situations where microbial species migrate faster than trees, or vice versa. This research will allow for more precise predictions about how forests will change as climates warm.

This research will involve citizen scientists from across the eastern US in collecting samples for the soil survey. Several undergraduate students will also be involved in performing the research. Finally, by helping to improve our ability to predict ecological changes in response to climate change, this research will increase our ability to mitigate and adapt to the undesirable consequences of a rapidly warming world.



Above: External hyphae of arbuscular mycorrhizal fungi with spores growing around sycamore (*Platanus occidentalis*) roots.

Below: Arbuscular mycorrhizal fungi colonizing a sycamore (*Platanus occidentalis*) root. Thin blue lines are hyphae, blue ovals are vesicles (storage structures), and dark blue rectangles are arbuscles, the site of nutrient exchange between the plant and fungus. Plants and mycorrhizal fungi have a mutualistic relationship, in which the plant provides sugars to the fungus in exchange for soil nutrients (especially phosphorous).



Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host

Carol Lee, University of Wisconsin Madison (NSF 1046372); Joana Carneiro da Silva, University of Maryland at Baltimore (NSF 1046371)

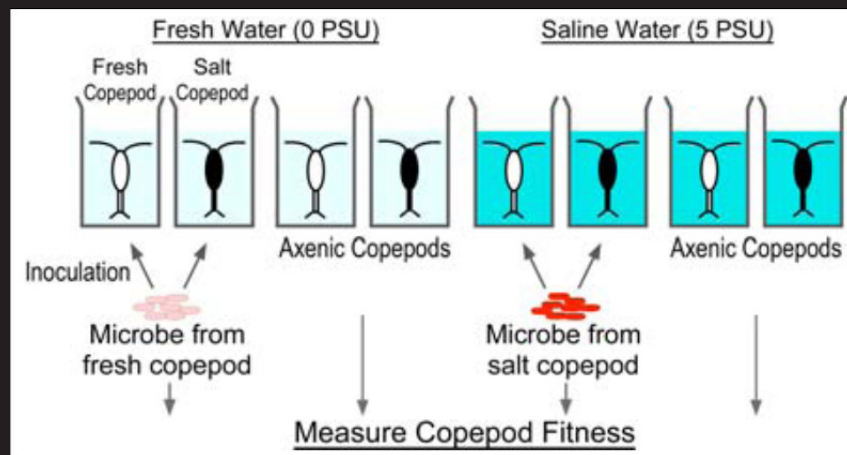
This project characterizes diversity and metabolic functions of the microbiome of a copepod, and will test how the diversity and functions (metabolic and ecological) change when the saline copepod invades a novel habitat (fresh water).

Copepods form the largest biomass of metazoans on the planet, yet their microbiota remain largely unexplored. The microbial community associated with copepods might perform key metabolic processes that affect host fitness and ecosystem functioning. The copepod *Eurytemora affinis* is dominant in coastal habitats throughout the world, and recently has invaded inland freshwater habitats. Associated with *E. affinis*, preliminary sequencing revealed high diversity of microbial taxa, including many undescribed genera and families. There also were parallel shifts in microbial composition during independent invasions from saline to freshwater habitats. Yet, a core set of microbial taxa remained present in all copepod populations across all locations. The copepod microbiome is likely to play fundamental roles in biogeochemical processes in many aquatic ecosystems. Microbial-host interactions could influence invasive success, and exotic microbes in the invading consortia could have vital impacts on the invaded community. This study will address the taxonomic composition of the copepod microbiome, and how it shifts during habitat invasions; the metabolic functions performed by the copepod microbiome; and the nature of copepod host-microbial interactions, and how these interactions shift during invasions. Preliminary sequencing of the *E. affinis* microbiome uncovered a wide

variety of potentially pathogenic taxa, including *Salmonella*, *Shigella*, *Campylobacter*, *Corynebacterium diphtheriae*, *Yersinia*, and *Vibrio cholerae*. Thus, *E. affinis* might play an important role as a reservoir and vector of waterborne disease. This collaborative research will be promoted through workshops that integrate diverse perspectives across fields, such as microbial ecology, disease ecology, ecosystem ecology, and evolutionary biology. The project will also involve an internship program for underrepresented students to partake in genomic data analysis and an annual public symposium on applied evolution, including a teacher-training workshop at the high school level. This project will support one postdoc, and up to two graduate and three undergraduate students per year, including those from underrepresented backgrounds.

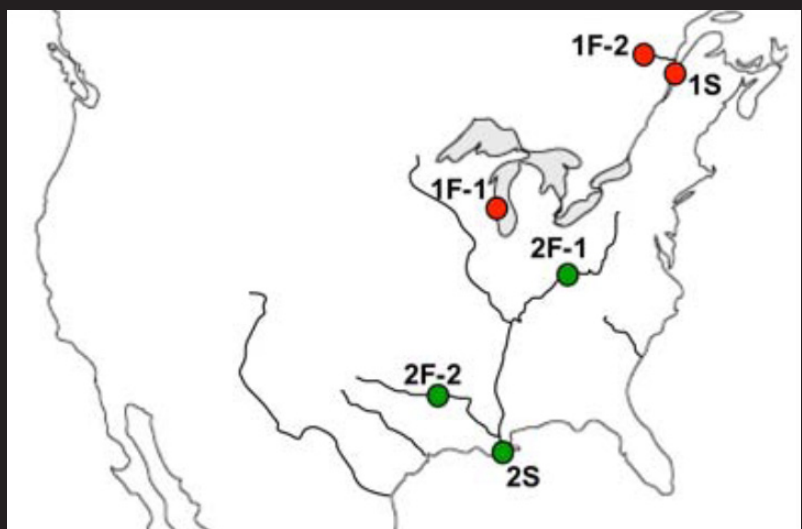
This study will provide integrated insights into the taxonomic, genetic, and functional diversity of the copepod microbiome. The assembled sequences will link specific metabolic functions with particular microbial taxa, illuminating functional diversity across deeply divergent lineages. Sequence data also will reveal genetic diversity of metabolic functions within microbial taxa, and the potential sharing of functions across taxa (e.g. via horizontal gene transfer).

Right: The coastal copepod *Eurytemora affinis*. This copepod is a dominant grazer of algae and a major food source for some of the world's most important fisheries, such as herring, anchovy, salmon, and flounder.



Left: A factorial test of copepod response to microbes. The scientists will measure copepod host fitness (e.g. egg production, development time, survival) in response to the microbes relative to axenic conditions.

Right: Population sampling of *Eurytemora affinis* for the preliminary study and proposed research. Sampling includes saline and freshwater populations, from two genetically distinct clades (red, green). Sampling captures independent invasions from saline into freshwater habitats.



An interdisciplinary study of hyperdiverse endophytic fungi and their function in boreal forests

Francois Lutzoni, Duke University (NSF 1046065); Anne Arnold, University of Arizona (NSF 1045766); Ignazio Carbone, North Carolina State University (NSF 1046167); Georgiana May, University of Minnesota, Twin Cities (NSF 1045608)

This project will look at a diverse and poorly described group of endophytic fungi with symbiotic relationships to boreal vascular plants and lichens.

The global diversity of fungi is estimated to far exceed 1,500,000 species, yet mycologists have described only about 100,000 species. This disparity reflects an immense richness that is hidden within symbiotic organisms. Symbioses drive ecological diversification, genome evolution, and speciation, shaping all dimensions of the diversity of life. The goal of this project is to study one of the planet's most prevalent but least-understood symbioses: that of *endophytic fungi* (*endophytes*), which occur within healthy above-ground tissues of all plants in biomes ranging from tropical rainforests to Arctic tundra.

Endophytes comprise as many as 1 million species, less than 1% of which have been described to date. They have been found in every plant and lichen species, including wild-, crop- and forage plants, and their communities often change markedly across hosts' geographic ranges. Endophytes produce metabolites of use in agriculture, medicine, and industry, and can provide defense against pests and pathogens, and tolerance to heat and drought. Endophytes peak in phylogenetic diversity in boreal forests, an ecosystem of immense global importance and one in which their ecological associations, genetic diversity, and functional roles are largely unknown.

The goal of this project is to develop a biodiversity-informatics pipeline to describe the taxonomic, functional, and genetic diversity of endophytes at

multiple scales. As a result, the scale of endophyte biodiversity will be unveiled for the world's largest biome, transformative taxonomic practices to capture unknown diversity will be established, new and useful model systems for functional and genetic studies will be developed, biological functions of endophytes will be tested systematically through experimental work, and the mechanisms underlying the genetic and functional diversity of these hyperdiverse symbionts will be elucidated.

Every component of this proposal, including the core hypotheses driving it, resulted from fusion of the complementary strengths of the PI team and an international network of collaborators in taxonomic, genetic, and functional biology. The result is an exquisite opportunity to address ecological, evolutionary, and mechanistic questions in a synthetic manner far exceeding the scope of any individual lab. Innovative training of STEM teachers, high school, undergraduate, and graduate students, and postdoctoral fellows both locally and abroad will contribute to a broader understanding and appreciation of the boreal biome, the roles of cryptic fungal symbionts, and the scope and importance of Earth's undiscovered biodiversity.

Bascom-Slack, C., A.E. Arnold, S.A. Strobel. 2012. Student-directed discovery of the plant microbiome and its products. *Science* 338: 485-486.

Olarte, R.A.; Horn, B.W.; Dorner, J.W.; Monacell, J.T.; Singh, R.; Stone, E.A.; Carbone, I. 2012. Effect of sexual recombination on population diversity in aflatoxin production by *Aspergillus flavus* and evidence for cryptic heterokaryosis. *Molecular Ecology* 21:1453-76.

A. Survey sites for endophytic fungi in the circumboreal biome: blue stars, sampling complete (2011-2012); yellow stars, sampling sites for 2013. **B.** Project logo and website URL. **C.** Sampling sites in Québec, Canada, with sites marked along ca. 900 mi transects from the southern to northern extent of the boreal biome, and at increasing inter-site distances on a single latitudinal band. **D.** Lichens at field site in Alaska. **E.** Project postdoc Jana U'Ren collecting in Alaska. **F.** Project postdocs Valerie Wong and Ryoko Oono processing specimens. **G.** Project postdoc Emilie LeFevre leading the field team from the floatplane used to access sites in Québec. **H.** Senior scientist Jolanta Miadlikowska collecting lichens in Sweden. **I.** Emilie LeFevre, assistant Kayla Arendt, and Jolanta Miadlikowska in the field near the northern edge of boreal forest in Québec. **J.** Fungal endophyte growing on nutrient medium. **K.** Phylogenetic richness of boreal endophytes relative to those in other biomes. **L.** Fungal endophyte growing on nutrient medium.



Biological controls in the ocean: The Redfield Ratio

Adam Martiny and Steven Allison, University of California Irvine (NSF 1046297); Simon Levin, Princeton University (NSF 1046001); Michael Lomas and Benjamin Van Mooy, Bermuda Institute of Ocean Sciences (NSF 1045966); and Kun Zhang, University of California San Diego (NSF 1046368)

The Redfield ratio is the ratio of nitrogen to phosphorus in seawater. Understanding how biodiversity regulates the Redfield ratio will provide important insights for understanding the role of biodiversity in regulating global nutrient cycles.

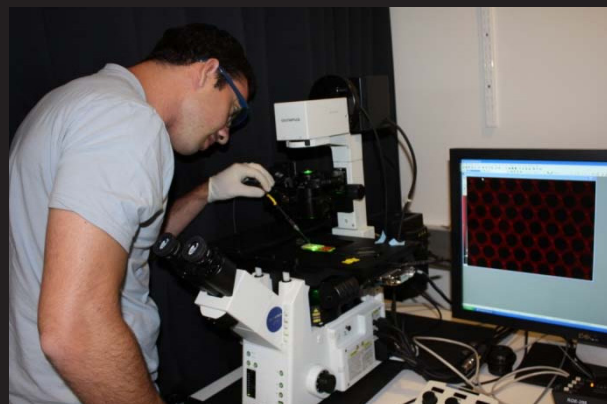
Decades ago, Alfred Redfield observed that the ratio of nitrogen-to-phosphorous in ocean surface plankton matched the ratio of dissolved nitrogen-to-phosphorous in the deep ocean. Furthermore, this ratio was constant all over the ocean. Redfield proposed that the hydrolysis of sinking surface particles controlled the deep ocean chemistry and this hypothesis remains a central tenet for our understanding of ocean biogeochemistry. There is, however, substantial elemental variation among plankton species as well as communities in different ocean regions. This led the investigators to propose that the biodiversity of ocean plankton regulates the elemental composition of the ocean and differences in biodiversity can lead to substantial deviations in the nitrogen-to-phosphorous ratio.

This project will measure the *in situ* elemental composition of abundant plankton lineages in different ocean regions. The investigators will apply a novel

technique combining fluorescence activated cell sorting with high-sensitivity elemental analysis to achieve this. Simultaneously, they will identify variations in biodiversity using next-generation high-throughput sequencing technologies and single-cell genome sequencing. Finally, a series of controlled laboratory experiments will be used to delineate specific effects of environmental variation versus changes in biodiversity on the elemental composition of a plankton community. The researchers aim to understand how ocean taxonomic (i.e. different lineages), genetic (difference in genome content within a lineage), and functional (i.e. ability to use particular food sources) biodiversity integrate to control chemical composition of the ocean. Beyond significantly advancing our basic understanding of biodiversity, the study will also provide important new information of how ocean plankton can control major nutrient cycles.

J.A. Bonachela, M. Raghib, and S.A. Levin. 2011. Dynamic Model of Flexible Phytoplankton Nutrient Uptake. *PNAS* 108: 20633.

This paper introduces a new model describing the ability of phytoplankton to acclimate to environmental changes by altering the cell's nutrient uptake strategy. The model incorporates explicitly the regulation of phytoplankton uptake proteins. The authors show that this plasticity, not present in standard models for nutrient uptake, allows phytoplankton cells to increase uptake and growth rates, which enhances their survival probability especially in oligotrophic conditions. Flexible models like the one presented in this article may help improve, for instance, models for the oceanic biogeochemistry, which lack the description of this regulatory mechanism.



Above: A student from co-PI K. Zhang's laboratory using a microfluidic chip to amplify and pick single-cell genomes

Left: A sampling rosette from R/V *Atlantic Explorer* Dimensions of Biodiversity project.

Below left: Members of PI A. Martiny and co-PI S. Allison laboratories at the sampling site at Newport Pier, California

Below right: Co-PI Lomas participates in the outreach program "crush-a-cup" aboard the R/V *Atlantic Explorer*



All Images: Adam Martiny, University of California, Irvine

Genomics, functional roles, and diversity of the symbiotic gut microbiotae of honey bees and bumble bees

Nancy Moran, Yale University; and Jay Evans, USDA ARS (NSF 1046153)

Most of Earth's biodiversity is microbial. This project will examine the microbiota in the guts of bees from two genera—Apis (honey bees) and Bombus (bumblebees). The research will offer important insights into the ecological resilience of organisms that provide economic, ecological, and agricultural value through their pollination services.

All animals live in close association with microbes, primarily bacteria, and the large majority of these bacteria are not associated with disease. The gut is especially rich in diverse lineages and species of bacteria. These have been studied in only a few host species, in which they have been shown to benefit particular hosts by assisting with digestion of food, provisioning essential nutrients, and enhancing defenses against pathogens. The diversity and functional roles of gut microbiota are almost entirely unknown for most species. Also, little is known of how environmental change impacts gut bacteria and consequently the hosts themselves.

The focus of this project is the diversity, functional roles, and genetic diversity of bacteria living in the guts of honey bees and bumble bees. As dominant pollinators, these insects are critical players in terrestrial ecosystems, including agricultural systems. Furthermore both honey bees and bumble bees have experienced population declines in recent years, and better understanding of their basic biology and of the impact of environmental change is essential to addressing these declines. The honey bee is a single species introduced nearly worldwide for the production of honey and for pollination of crops. Worldwide, honey bee adults contain a distinctive set of bacterial types in their guts, and bumble bees contain some related bacterial species. Using the latest technology, the genome

sequences of these bacteria will be obtained and analyzed to characterize their metabolic capabilities and their potential functions in hosts. Further experiments will measure the impact of bacterial presence on the health of honey bees. The impact of environmental variation on the diversity and composition of the microbiota will be assessed by using high throughput DNA sequencing to compare microbiota from honey bees worldwide, and from selected species of bumble bees in North America and in China, the regions with the highest bumble bee diversity globally. In particular, the impact of different human-mediated changes will be assessed by comparing the gut microbiota of bees from agricultural and other sites with different management practices.

By analyzing these impacts in the context of knowledge of the functional roles of these bacteria, possible linkages between anthropogenic environmental changes and the health of bee populations will be assessed. Because the work combines methods from genomics, experimental biology and ecology, the research team is interdisciplinary and includes scientists from both academic institutions and government agencies. This research will be integrated into a high school science education program, organized by the Yale Peabody Museum for New Haven students.

Martinson, V.G., J. Moy, and N.A. Moran. 2012. Establishment of characteristic gut bacteria during development of the honey bee worker. *App and Env Microbiology* 78:283.
Moran, N.A., A.K. Hansen, J.E. Powell, and Z. Sabree. 2012. Distinctive gut microbiota of honey bees assessed using deep sampling from individual worker bees. *PLoS ONE* 7(4).
Engel, P., Martinson, V.G., and N.A. Moran. 2012. Functional diversity within the simple gut microbiota of the honey bee. *Proc Natl Academy of Sciences USA* 109:11002.



Jay Evans, USDA



Waldan Kwong, Yale University

Far left: Honeybee workers on the hive (*Apis mellifera*)

Left: Honey bee queen being tended by her workers on the comb



N. Moran



Nancy Moran, Yale University

Right: Common eastern bumblebee, *Bombus impatiens*, on aster

Far right: Sonoran bumblebee, *Bombus sonorus*, on hibiscus



Kim Hammond, Yale University

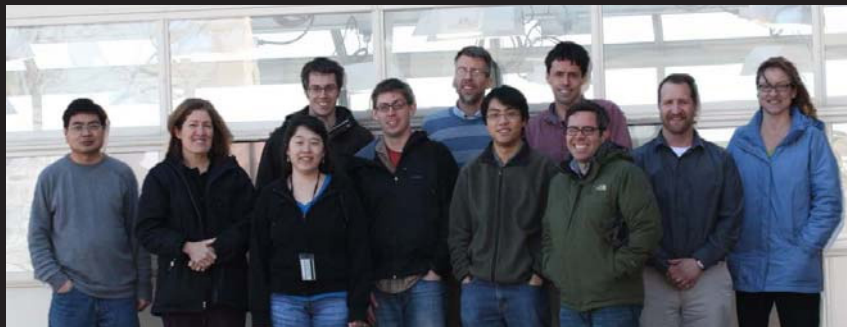
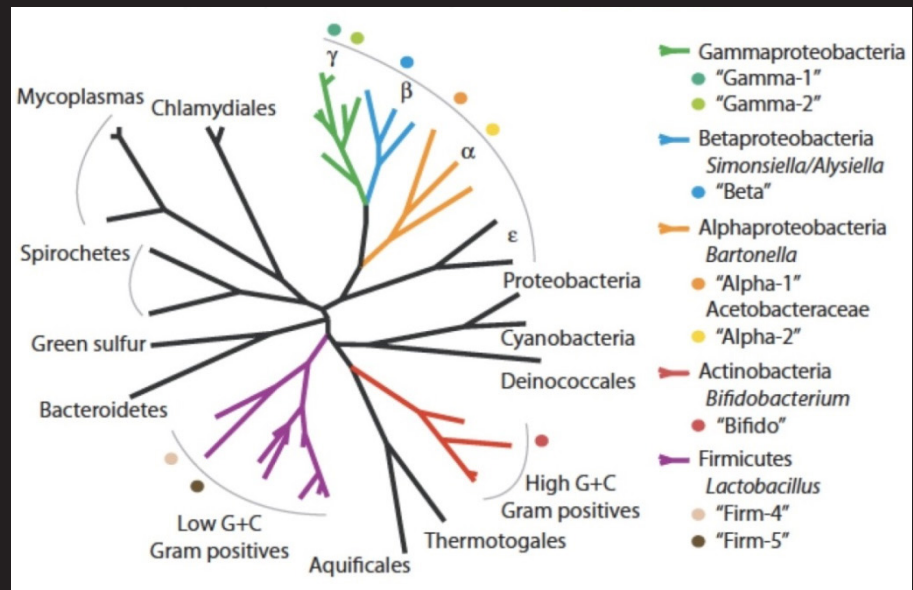
Left: Graduate students netting honey bees in order to sample the bee gut microbiota

Right: Researchers removing bee pupae from comb in the laboratory



K.Hammond

Right: Relationships of bacteria known to live in honey bees



N. Moran

Vince Martinson, University of Arizona

Left: Bee microbiota researchers at planning meeting in New Haven Connecticut

An integrative traits-based approach to predicting variation in vulnerability of tropical and temperate stream biodiversity

N. Leroy Poff, William C. Funk, Cameron Ghalambor, and Boris Kondratieff, Colorado State University (NSF 1046408); Alexander Flecker, Joseph Bernardo, and Kelly Zamudio, Cornell University (NSF 1045960); and Steven Thomas, University of Nebraska Lincoln (NSF 1045991)

Predicting the effects of rapid climate change on biodiversity is an important and urgent scientific challenge. This project will examine the influence of climate change on stream biodiversity in a tropical stream system in the Andes of Ecuador and a temperate alpine stream system in the Colorado Rockies.

Predicting the consequences of rapid climate change on biodiversity loss and ecosystem function is an urgent scientific challenge. Species responses will reflect both the magnitude of environmental change and their relative sensitivity to that change. In this project the investigators will develop a new conceptual framework that integrates evolutionary, ecological, and physiological perspectives, unifies disconnected themes of biodiversity theory, and experimentally quantifies mechanisms of species vulnerability and ecosystem sensitivity to warming and increased variation in precipitation. The research will take place in small streams that occur along a broad elevational gradient in the Colorado Rockies and the Ecuadorian Andes.

Theory predicts tropical stream species (aquatic insects, frogs, and fish) should be more sensitive to a unit increase in warming than temperate species because tropical species have evolved in thermally stable habitats. As climate warms, species will either need to move to higher elevations, and/or exhibit physiological adjustments to tolerate changing environmental conditions. Species vulnerability to rapid climate change will reflect a complex interplay of physiological response to warming, capacity to disperse to favorable habitats and ecological sensitivity to modified disturbance and ecosystem processes.

To test predictions arising from these interactions, the investigators will use genetic techniques to discover new species and assess their ability to move between streams as climate changes; physiological techniques to experimentally measure tolerance of species to warming and reduced oxygen; and ecological experiments that conduct whole system manipulations of disturbance regimes and oxygen levels in sensitive alpine streams.

This study will provide a novel, integrative model for predicting species and stream ecosystem responses to climate shifts. It will advance fundamental knowledge of tropical stream diversity required to understand vulnerability of these systems to rapid climate change relative to mid-latitude temperate streams. By combining results from field surveys and experiments with projected future scenarios of temperature and precipitation change, this study will be the first to map spatial variation in stream species and ecosystem vulnerability across latitude and elevation gradients in multiple taxonomic groups (aquatic insects, frogs, and fish) and thus will be highly relevant to policy makers concerned with freshwater biodiversity conservation and sustainable water management.



Left: A waterfall and stream located near the Mindo Biological Station at about 1700 m (Pacific versant of the Ecuadorian Andes)

Right: Investigators Ghalambor and Poff investigate the contents of a Hess sample while scouting creeks in Ecuador



Below right: *Nymphargus wileyi*, a holotype of a new species of centrolenid (glass frogs) that PIs discovered & described at Yanayacu Biological Station at ~2000 m (Amazonian versant of the Ecuadorian Andes)



Below left: A transect is laid along a creek at one of the Colorado Bioblitz sites

Below center: PhD student, Brian Gill searches his aerial net for adult aquatic insects at a high elevation site in the Colorado Rockies

Below Right: A vial of stoneflies collected at 3400m in the Colorado Rockies



Below: US investigators and Ecuadorian collaborators in Ecuador, March 2011



All Images: W. Chris Funk, Colorado State University

Shedding light on viral dark matter–genetic, taxonomic, and functional diversity of coral reef viromes

Forest Rohwer, Robert A. Edwards, and Anca Segall, San Diego State University (NSF 1046413)

This project will examine virus diversity on coral reefs along a gradient of human-caused effects at both regional and global scales.

Viruses are the most abundant, most diverse, and least understood biological entities on Earth. It is very likely that the most common organism on the planet is a virus that is currently unknown to science. Because viruses reproduce within a host cell, they can have enormous impacts on the well being of the host and possess genes that are integral to the host's ability to carry out important biological functions, such as photosynthesis in marine environments. A major goal of this research project is to develop novel high-throughput methods to rapidly reveal and characterize the diversity of this biological "dark matter". First, the size of the global viral gene pool will be determined by analyzing viral DNAs from the world's major biomes. The work will then focus on the viruses of coral reefs by examining the most abundant viral proteins and determining

their functions using genetics and protein structures. Combined and integrated, these approaches will address the genetic, functional, and taxonomic dimensions of viral biodiversity.

Discoveries stemming from the study of viruses have been at the forefront of many breakthroughs in biological research. Values to society from this specific work will include more comprehensive knowledge of global viral biodiversity and of the role of viruses in the health of coral reefs—valuable ecosystems that are under considerable stress due to climate change and other human activities. It is expected that this research will improve our fundamental understanding of the interactions of viruses, human activities, and the biodiversity of the planet.

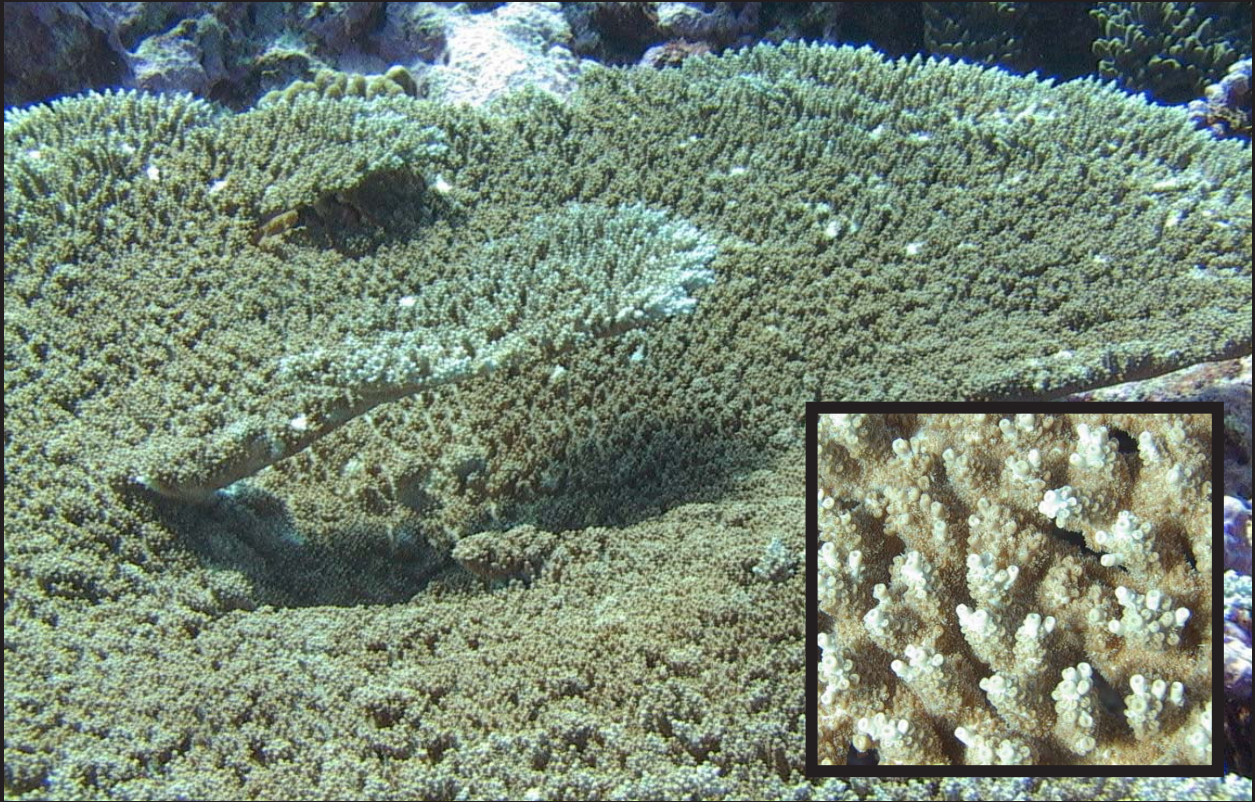
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Aziz, R.K., S. Devoid, T. Disz, R.A. Edwards, C.S. Henry, G.J. Olsen, R. Olson, R. Overbeek, B. Parrello, G.D. Pusch, R.L. Stevens, V. Vonstein, and F.F. Xia. 2012. SEED servers: high-performance access to the SEED genomes, annotations, and metabolic models. *PLOS One* 7(10).

Coral reefs are among the most complex and diverse biological systems on Earth. Dr. Rohwer's lab uses metagenomics to study the microbial and viral communities inhabiting coral reefs.



Above: *Acropora* sp. with closeup of polyps (inset)

Below: Dr. Rohwer sampling corals



All Images: Forest Rohwer

Parallel evolutionary radiations in Protea and Pelargonium in the Greater Cape Floristic Region

Carl Schlichting, Kent Holsinger, Cynthia Jones, and John Silander, University of Connecticut (NSF 1046328); Andrew Latimer, University of California Davis (NSF 1045985); Justin Borevitz, University of Chicago (NSF 1046251)

The fynbos and succulent karoo biomes in South Africa's Greater Cape Floristic Region are two of the world's plant biodiversity hotspots. Using these two plant genera as model systems, this project will look at the ways in which functional diversity of traits evolves and influences community dynamics.

Rapidly changing climate will drive dynamic responses at all levels of biodiversity, from the traits of individuals to distributions of species and biomes. Current approaches to predicting such responses are based on static assessments, e.g., what is a species' current ecological envelope and where will that range of conditions occur in the future? This project will expand the information used for evaluating such responses to include: a) relationships between species' attributes that affect their function in a given environment (functional traits), b) genetic variation underlying those functional traits, and c) the dynamics of the communities of which they are part. The investigators also suggest that studies of clades that have evolved and flourished through dramatic historical climate change may be able to provide significant information about the evolution of functional traits and the potential for further adaptive evolution.

Southern Africa possesses higher plant diversity than most tropical regions, yet much of this diversity stems from radiations in just 30 major lineages. This research will focus on two highly successful plant genera, *Protea* (112 spp) and *Pelargonium* (280 spp), that have diversified over the past 15 MY in response to, or in spite of, radical (and at times rapid) changes in the climate of southern Africa.

These genera span two biodiversity hot spots, the fynbos and succulent karoo biomes in the Greater Cape Floristic Region (GCFR). Over 65% of GCFR plant species are endemic, an extraordinary level for a continental region. The goal is to develop an understanding of variation of functional traits (e.g. leaf size and shape, leaf longevity, photosynthesis, and water use) in both genetic and evolutionary contexts in *Protea* and *Pelargonium* at intraspecific and community levels. This will allow the investigators to predict the characteristics of communities in which they occur and the resilience of those communities to climate change.

This integrated team has expertise in a wide range of ecological and botanical disciplines and the project will expose post docs, grad students, undergrads and high school students to international research, including students actively recruited from underserved populations both in the US and South Africa. The project will host annual methods workshops and actively enhance conservation infrastructure by working closely in all aspects of the project with the South African National Botanical Institute (SANBI) which has one of the best track records in the world in promoting biodiversity science, policy and conservation action.

Martinez-Cabrera, H.I., C.D. Schlichting, J.A. Silander, and C.S. Jones. 2012. Low levels of climate niche conservatism may explain clade diversity patterns in the South African genus *Pelargonium* (Geraniaceae). *American Journal of Botany* 99:954-960.

Proteas, the national flower of South Africa, are key inhabitants of the Fynbos biome, a Mediterranean shrubland of southwestern South Africa. Fynbos is critically threatened by climate change.



Jane E. Carlson, University of Connecticut



J.E. Carlson



J.E. Carlson

Left: *Protea aurea*, Blesberg, Western Cape Province, South Africa

Above center: *Protea cyanaroides*

Above right: *Protea venusta* Pelargoniums

(Below) are the ancestors of cultivated 'geraniums'. These plants are marked by their diversity in growth form, leaf shape and flower types



Carl D. Schlichting, U. of Connecticut



Cynthia S Jones, U. of Connecticut



C.D. Schlichting

Far left: *Pelargonium crithmifolium*

Center Left: *Pelargonium exhibens*

Left: *Pelargonium peltatum*



C.D. Schlichting

Left: *Pelargonium sericifolium*

Right: Fieldwork in South Africa with bontebok (*Damaliscus pygargus pygargus*)



C.S. Jones

Significance of nitrification in shaping planktonic biodiversity in the ocean

David Stahl, E. Virginia Armbrust, Allan Devol, and Anitra Ingalls, University of Washington (NSF 1046017); James Moffett, University of Southern California (NSF 1046098)

This project examines the diversity and function of ammonia oxidizing Archaea in the ocean and the role of these newly discovered organisms in structuring the diversity of phytoplankton.

Microorganisms sustain the nitrogen cycle, one of the most important nutrient cycles on earth. Agriculture and industry have profoundly altered the nitrogen (N) cycle, increasing biologically available nitrogen, with uncertain impacts on terrestrial and marine systems. A key step in the (N) cycle, the microbial oxidation of ammonia to nitrite, was long thought to be mediated by a few genera of bacteria. It is now known that much, if not most, ammonia oxidation is due to the activities of a group of microorganisms affiliated with the *Archaea*.

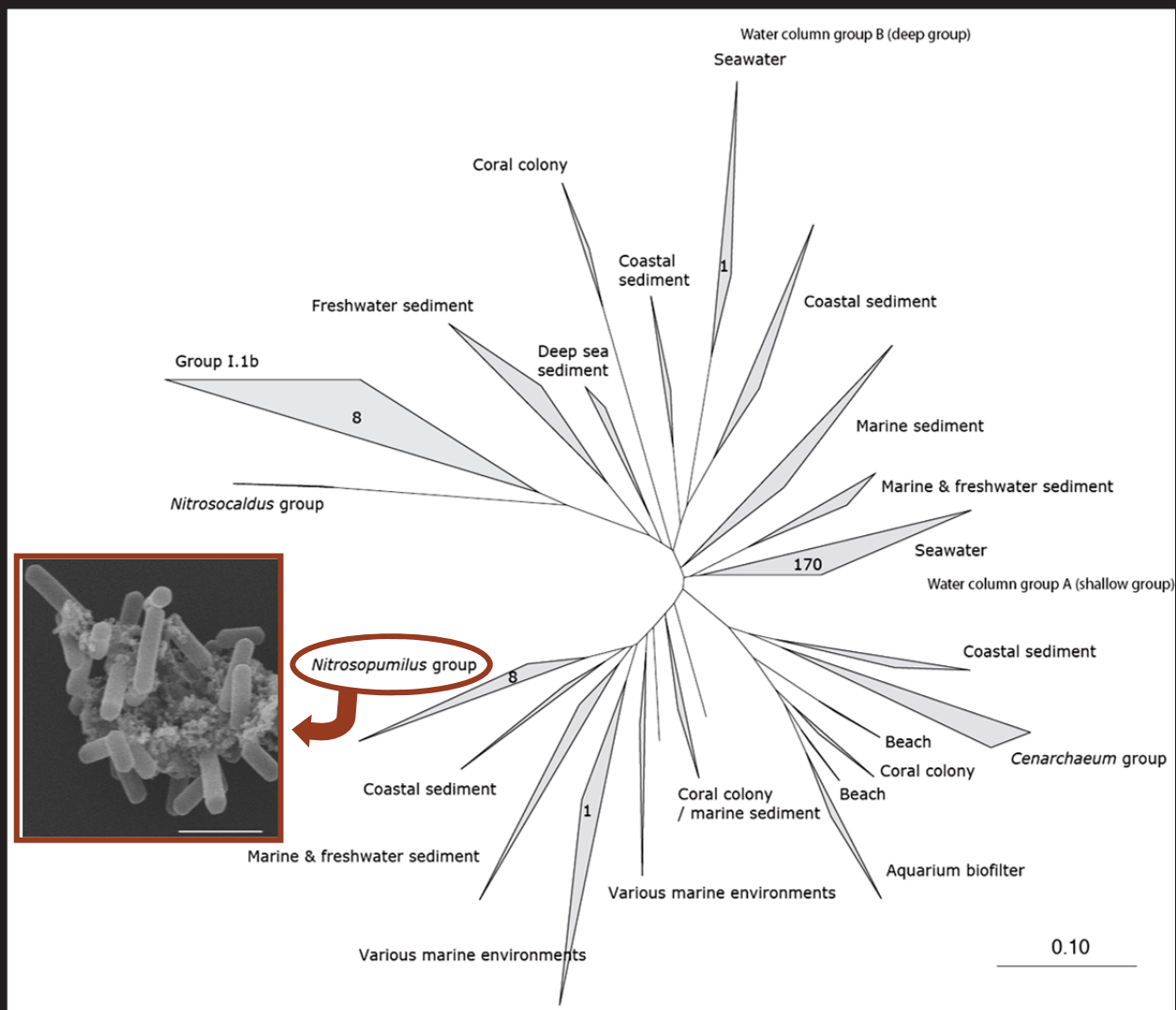
The single-celled *Archaea*, together with bacteria and eukaryotes, are the three primary evolutionary lineages on earth. Although *Archaea* are abundant in the oceans, they have only recently been directly associated with nitrification, the oxidation of ammonia (released primarily through decay of other organisms) to nitrite and nitrate. Prior analyses of marine ammonia-oxidizing *Archaea* (AOA) has shown that AOA are active within the marine photic zone and that their high abundance is in part attributable to an extremely high affinity for ammonia. The AOA can sustain near maximum growth rates at a concentration of ammonia equivalent to 1 teaspoon of ammonia diluted into 50,000 gallons of water. The compelling inference is that AOA may control the forms of nitrogen available to other microbes within the photic zone by converting ammonia, a nearly universally available form of nitrogen, into nitrite, a form only available to nitrite oxidizing bacteria and some phytoplankton.

In addition to their ability to deprive other marine organisms of ammonia, genetic analyses point to an unusual copper-based system of respiration that may render them more competitive in iron limited environments. The implication is that AOA have a significant impact on marine biodiversity, primary production, and the release of atmospherically active gasses such as nitrous oxide.

The project encompasses and integrates the three dimensions (functional, genetic, and taxonomic) of biodiversity. The project is framed by function: microbial control of the nitrogen-cycle. It is motivated by recent genetic analyses that associate activities of a novel clade of *Archaea* with control of ammonia oxidation in the ocean. It is built upon a compelling synthesis of physiological and environmental data that lead to its central hypothesis—that by altering and possibly controlling the form of nitrogen, the AOA also alter biodiversity and ecological function in one of the most productive environments on earth. It addresses a specific taxonomic imperative. The tremendous genetic diversity among the globally abundant AOA – catalogued almost exclusively by gene sequencing surveys and therefore lacking formal description – makes it essential to resolve membership into ecologically relevant groups or clades as a prelude to developing a formal taxonomy. Outreach programs will enhance understanding among students and teachers of the role of microorganisms in global elemental cycles such as the N cycle.

Metcalfe, W.W. et al. Synthesis of methylphosphonic acid by marine microbes: a course for methane in the aerobic ocean. *Science* 337:1104-1107.

Merbt, S.N., D.A. Stahl, E.O. Casamayor, E. Marti, G.W. Nicol, and J.I. Prosser. 2012. Differential photoinhibition of bacterial and archaeal ammonia oxidation. *FEMS Micro Letters* 327:41-46.



Above: Diversity of ammonia oxidizing archaea inferred by sequencing a gene (*amoA*) required for the oxidation of ammonia

Inset above: Scanning electron micrograph of *Nitrosopumilus maritimus*, the first marine ammonia oxidizing archaeon isolated in pure culture; Scale bar = 1 μm

Right: Deployment of instrumentation for analysis of the microbial and chemical structure of Hood Canal (Washington State), one of the field sites for the research project



All images: David A. Stahl, University of Washington

The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

David Valentine, University of California, Santa Barbara (NSF 1046144)

Microbes in ocean sediments form a unique ecosystem. There methane is consumed, preventing large amounts of this potent greenhouse gas from entering the atmosphere. The research will shed light on a dark corner of the biosphere, and could identify new and novel genes that support life in these environments. Methane (CH₄) is a potent greenhouse gas.

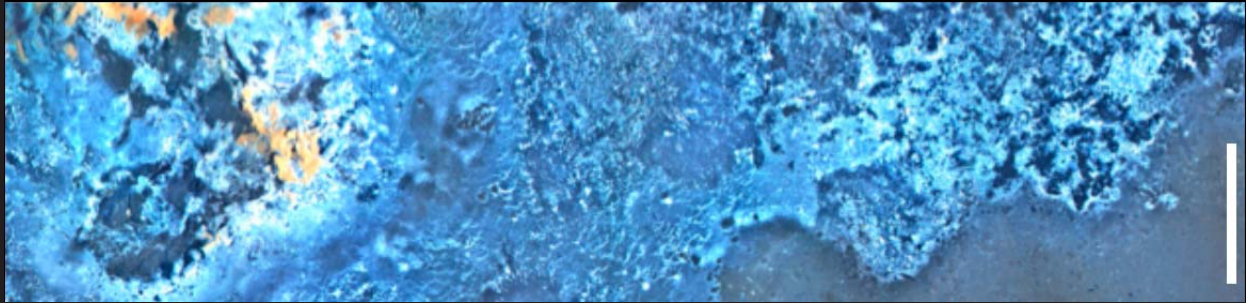
Ounce for ounce, over a hundred years, atmospheric methane will cause about 25 times as much global warming as carbon dioxide. About 550 teragrams (Tg) of methane enters the atmosphere each year – but without microbes, that number could be much higher. Some 85-310 Tg of methane is naturally produced beneath the world's oceans each year, and communities of methane-eating ("methanotrophic") microbes on the ocean floor consume all but about 10 Tg of it. By keeping so much methane from entering the atmosphere, these communities play an essential role in regulating global climate. And we know almost nothing about them.

What little we do know about these microbes explains why it has been so difficult to learn more. We know that they live on and in seafloor sediments, which complicates long-term observations. We know that they live an energy-starved life and this makes them grow very slowly, so they are particularly hard to culture for study onshore. We know that, while the oxygen-using (aerobic) methanotrophs from the shallow sediments are self-sufficient bacteria, the deeper, anaerobic methanotrophs are archaea that live in such close partnership with other microbes that they cannot be isolated and studied alone.

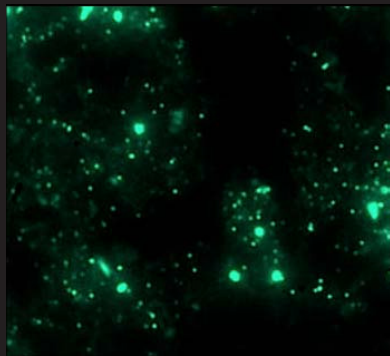
We also know that both the aerobic and the anaerobic microbial communities host huge viral communities – some ten times more viruses than hosts. The prediction that this project will test is that these

viruses, as agents of mortality and genetic transformation, fundamentally shape the biodiversity of the microbial methanotrophic communities. The research will address which microbes are merely present, and which actively consume methane; how diverse the active consumers are; whether the latent methanotrophs were once active; which viruses infect the active methanotrophs; whether viruses carry pirated microbial gene sequences, and whether these sequences have gotten shuffled back into the genomes of active methanotrophs; and how many viruses attack the active and latent methanotrophs. The investigators will use stable isotope probing (SIP) to acquire four separate pools of DNA fragments—from active methanotrophs, other microbes, viruses of active methanotrophs, and other viruses—and new sequencing technologies will be applied to these pools to learn which organisms and which genes are represented in each pool, whether host genes turn up in the viral pools, and how the pools differ in biodiversity. The researchers can also pick out intriguing individual cells and sequence their entire genomes. Comparing these individuals to the microbial communities they come from and the viral communities that preyed on them will provide an additional window into the community's history of genetic transfer and viral predation. Analyzing these data across different methanotrophic communities will tell us whether and how viruses influence the biodiversity of these essential microbes.

Below: Immense communities of methanotrophic microbes carpet the seafloor sediment at sites of natural methane seepage. Orange and white microbial mats grow at the Southwest Mounds, 900 m deep in the Santa Monica Basin off Los Angeles. Scale bar = ~1m



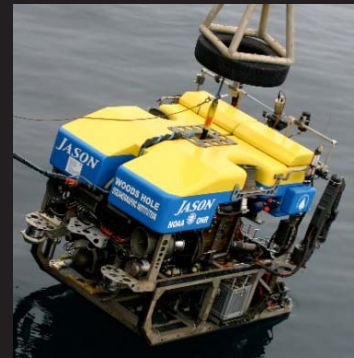
Oscar Pizarro, University of Sydney



Blair Paul, Univ. of Cal., Santa Barbara

Left: Epifluorescence microscopy shows viruses (green pinpoints) greatly outnumber bacteria (large spots) in a methanotrophic mat off Santa Barbara.

Right: ROV *Jason-2* is lowered with a payload of incubators to deploy and instruments to sample local biogeochemistry at the experiment's beginning.



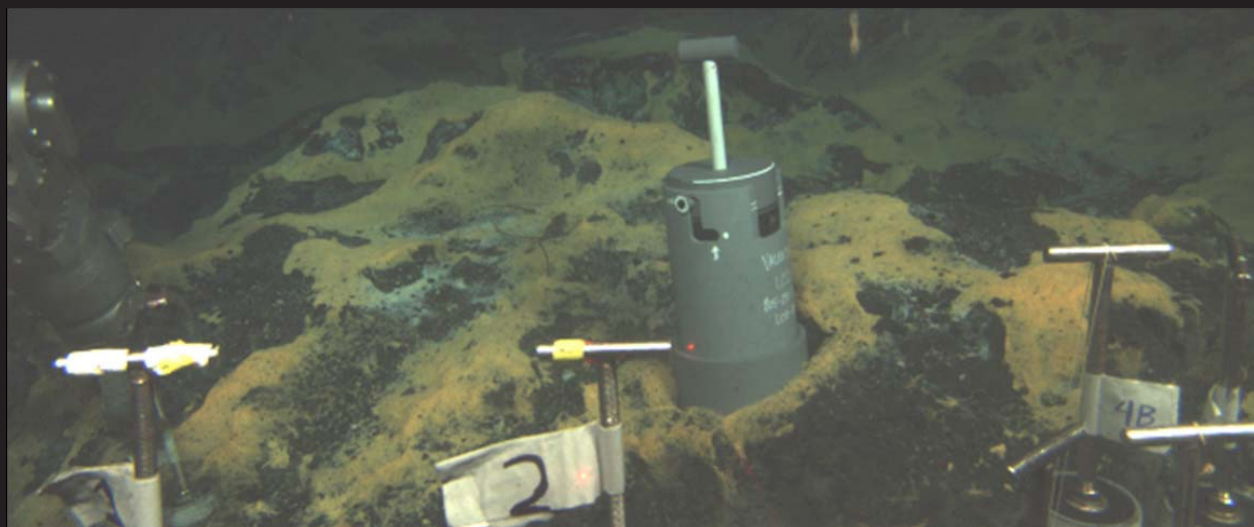
David Valentine, UC, Santa Barbara

Right: Side, bottom, and top views of aerobic methanotroph incubators. Incubators contain grids that support the growth of microbial mats (see below).



D. Valentine

Below: An incubator is deployed at the Southwest Mounds site, on the SEEPS September 2011 cruise (AT18-11). The top cap of the incubator will be left wide during initial deployment, allowing a natural community to develop. After two years the cap will be dropped, sealed in place, and injected with labeled methane for the *in situ* stable isotope probing (SIP) phase of the experiment. Several days later, the incubators will be brought to the surface for analysis.



D. Valentine

Roles of functional, phylogenetic, and genetic diversity in structuring and sustaining plant communities through environmental change

Donald Waller, Kenneth Cameron, Thomas Givnish, and Kenneth Sytsma, Univ Wisconsin-Madison (NSF 1046355)

Waller and colleagues are examining the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants in Wisconsin forests and grasslands. Their goal is to identify how climate change, habitat fragmentation, invasive species, and overabundant deer are acting to drive ecological change.

Shifts in the biodiversity of forests and prairies can often be tagged to changes like expanded numbers of browsing animals, invasions of exotic species, the loss and fragmentation of habitat, and accelerating climate change. In this project, the researchers will examine the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants occupying Wisconsin forests and grasslands. The project team seeks to determine trait evolution and community assembly in Wisconsin forests and grasslands; loss of native species and invasions by exotics over the past 50 years; and expected shifts in species distributions and community composition over the next 50 years related to climate and habitat change.

The research emphasizes how phylogeny influences the distribution of functional traits; how traits interact with sites to sort species among habitats; how traits interact with climate to influence present and future geographic ranges; and the extent to which population persistence reflects genetic variation, gene flow, dispersal, genome size, functional traits, and landscape conditions.

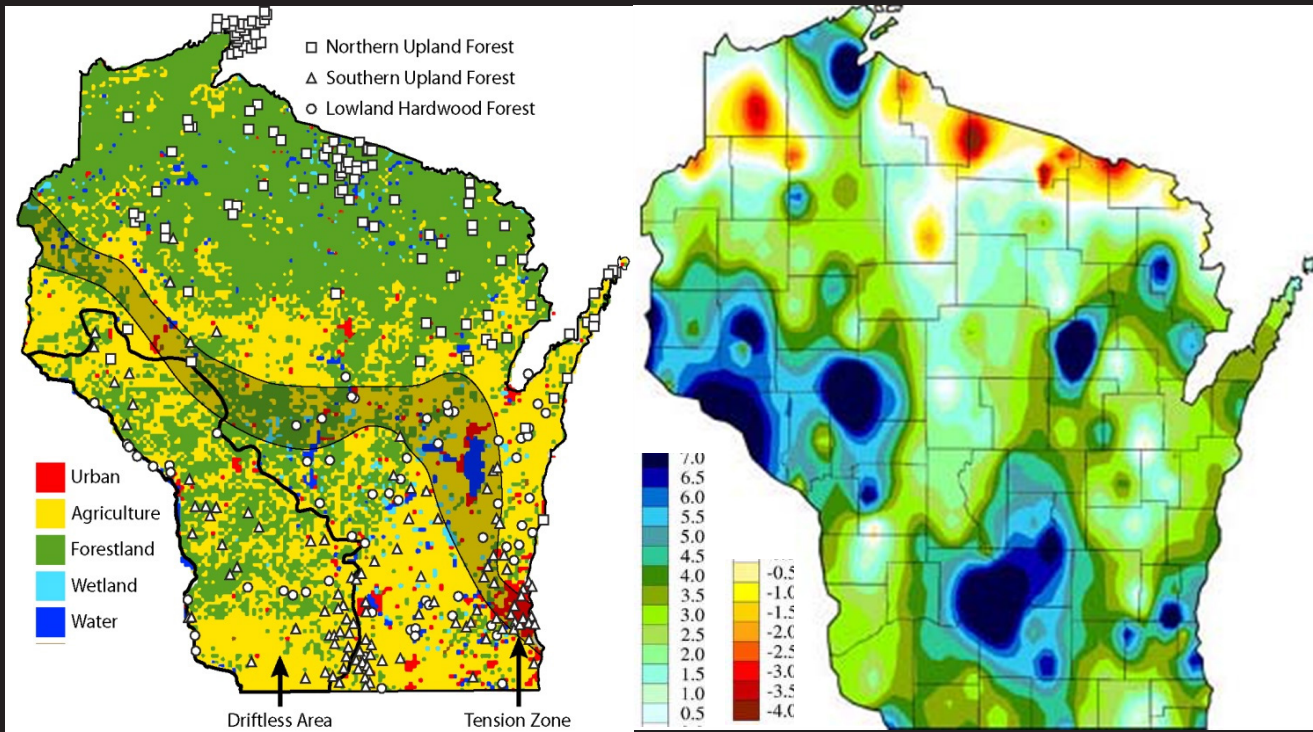
Key to this project is the work UW-Madison ecologist John Curtis and his students began in the 1940s, surveying sites throughout Wisconsin. This team

has resurveyed more than 350 forest and prairie plots, providing an exceptionally detailed picture of ecological change and ensuring that both spatial and temporal components are included in the project. The researchers are using genetic bar-coding – sequencing several key genes – to construct a phylogenetic (‘family’) tree for all 2,500 native and introduced plant species growing in Wisconsin. The tree will contribute to a wider “tree of life” for all North American plants and give the Wisconsin team a tool to analyze how phylogeny and diverging physical characteristics affect the distributions of plant species over sites. Several hundred species are being scored on up to 50 significant traits, allowing the researchers to judge their relative importance in determining plant distributions and changes in abundance.

Better understanding of patterns of genetic variation will help ecologists judge population vulnerability to further changes in landscapes and climate. Three of the world’s major biomes will be included in the research: deciduous forests, prairies, and coniferous forests.

Waller, D.M., K.L. Amatangelo, S. Johnson, and D. Rogers. 2012. Wisconsin Vegetation Database – Plant community survey and resurvey data from the Wisconsin Plant Ecology Laboratory. *Biodiversity and Ecology* 4:255.

Bai, Chengke, W.S. Alverson, A. Follansbee, and D.M. Waller. In press. New reports of nuclear DNA content 407 vascular plant taxa from the United States. *Annals of Botany*.



Donald Waller, Univ. of Wisconsin, Madison

From public domain *via* data visualization[†]

Above: Map of the Wisconsin J.T. Curtis forest sites that have already been re-surveyed by the team

Above: Change in precipitation (inches) in Wisconsin - 1950 to 2006



Grégory Sonnier, Univ. of Wisconsin, Madison

Left: A highly diverse prairie dominated by three plant families (Inset): Fabaceae (i.e. *Baptisia alba*), Asteraceae (i.e. *Rudbeckia hirta*), and Poaceae (i.e. *Andropogon gerardii*) (Dane County, Wisconsin, Summer 2011)

Right: A typical example of wind-dispersed species (*Tragopogon* sp., Asteraceae)

[†]Adapted from:

Kucharik, CJ *et al.* 2010. Patterns of climate change across Wisconsin from 1950 to 2006. *Physical Geography* 31: 1-28.

Wisconsin Initiative on Climate Change Impacts (WICCI). 2010. Maps from Climate Working Group. State of Wisconsin



G.Sonnier

Below left: Dr. Dave Rogers re-surveying an upland forest site in southern Wisconsin

Below right: Principal Investigators Ken Cameron, Don Waller, Ken Sytsma, and Tom Givnish (left to right)



D. Waller



D. Walle

Dimensions of Biodiversity Distributed Graduate Seminar

Julia Parrish, University of Washington (NSF 1050680)

Building on an innovative educational model, the Dimensions of Biodiversity Distributed Graduate Seminar seeks to prepare the next generation of biodiversity researchers for higher levels of academic and scientific interaction, while simultaneously advancing and synthesizing knowledge of biodiversity science on a global scale.

Distributed Graduate Seminars are an innovative approach to advancing science through an integration of research and education. The Dimensions of Biodiversity Distributed Graduate Seminar (DBDGS) focuses on increasing knowledge about biodiversity. The DBDGS will include 13 university teams, with international partners on three continents, and more than 100 students chosen from a wide range of disciplines needed to address biodiversity science (e.g., biology, geophysics, economics, computer science). The scientific goals of the DBDGS integrate across taxonomic, genetic, and functional approaches to biodiversity and are centered on two broad framing questions: (1) what forces create/maintain biodiversity pattern, and (2) what patterns of system function, service, or even associated human well-being does biodiversity drive? Each team is committed to using a meta-analytic approach with existing datasets from the literature and elsewhere, creating one or more academic products, and cross-fostering their ideas with other teams via web interactions and in-person synthesis meetings.

DBDGS will have a fundamental impact on this emerging field through its focus on the graduate student community, both nationally and internationally. Distributed seminars provide an intense team-driven, multi-disciplinary research experience that is likely to be important in future biodiversity research.

Because Core Team members represent both academic and non-governmental organization institutions, graduate students will also be exposed to a range of scientific career pathways. The DBDGS will foster international collaboration among young

scientists. Products of the seminar will be of interest to a broad range of researchers and will include open-access databases, student-led publications, and a symposium highlighting DBDGS findings at the Ecological Society of America annual meeting.

For more information: <http://www.dbdgs.org/>

Currently participating institutions (faculty leads):

United States:

Oregon State University (Selina Heppell)

University of California, Berkeley (Mary Firestone, Matt Potts)

University of California, Los Angeles (Sassan Saatchi)

University of California, Santa Barbara (Sandy Andelman, Jorge Ahumada, Sarah Lester)

University of Connecticut (Michael Willig)

University of Michigan (Brad Cardinale, Ivette Perfecto)

University of North Carolina (Allen Hurlbert, Charles Mitchell, Robert Peet)

University of Washington (Julia Parrish, Josh Tewksbury)

Virginia Institute of Marine Science (Emmett Duffy)

South America:

Pontificia Universidad Católica de Chile (Juan Armesto, Aurora Gaxiola, Pablo Marquet)

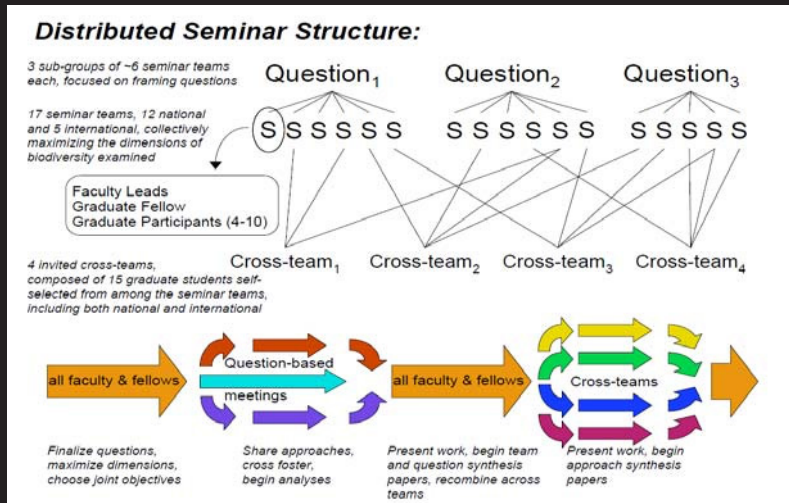
University Federal do Rio Grande do Sul (Valerio Pillar)

Asia:

Fudan University (Bo Li)

Africa:

East African Universities TBD (Alex Awiti)

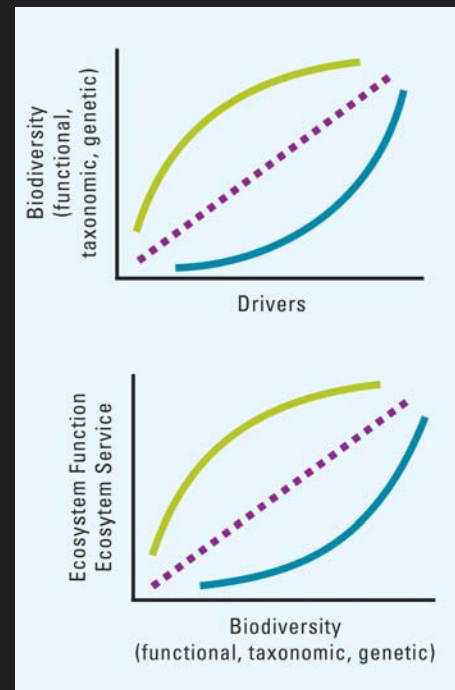


Julia K. Parrish, University of Washington

Right: DBDGS teams are addressing one of two broad framing questions:

- 1) What forces create/maintain biodiversity pattern, and
- 2) What patterns of system function, service, or even associated human well-being does biodiversity drive?

Left: The structure and schedule for the Dimensions of Biodiversity Distributed Graduate Seminar (DBDGS)



Cathy Schwartz



Cathy Schwartz

Left: DBDGS participating university teams

Below: DBDGS group photo taken at our February All-Hands Meeting at Friday Harbor Laboratories, University of Washington



Christina Maranto

International Research Coordination Network: Diversity and forest change: Characterizing functional, phylogenetic and genetic contributions to diversity gradients and dynamics in tree communities

US TEAM: Stuart Davies, Harvard University; Nathan G. Swenson, Michigan State University; W. John Kress, Smithsonian National Museum of Natural History; Rick Condit, Center for Tropical Forest Science, Smithsonian Tropical Research Institute (STRI); and Helene Muller-Landau, STRI (NSF 1046113)

CHINA TEAM: Zhanqing Hao, Institute of Applied Ecology, Chinese Academy of Sciences (CAS); Keping Ma, Institute of Botany, CAS; Wanhui Ye, South China Botanical Garden, CAS; Jie Li, Xishuangbanna Tropical Botanical Garden, CAS; Xiangcheng Mi, Institute of Botany, CAS; Xugao Wang, Institute of Applied Ecology, CAS

This project is the first to be funded by the partnership between NSF and the National Natural Science Foundation of China. A group of forest scientists from the US, China, and other parts of Asia has created an international research coordination network (IRCN) to explore the resilience of forests to global change.

This project will bring together two existing forest research networks in the US and China to advance understanding of how taxonomic, functional, and genetic dimensions of diversity structure tree communities and affect their resilience to global change. Together these teams maintain 42 large-scale forest plots in tropical and temperate forests in Asia and the Americas, providing data on the demography, functional traits, phylogenetic relatedness, and environmental preferences of thousands of species. Through a series of workshops and international scientific exchanges, these data will be used to ask: what functional traits underlie species demographics and distributions across environmental gradients; how do functional traits and phylogenetic relatedness of communities link to forest function; how do functional traits and environmental tolerances vary among individuals within species; and how does gene flow contribute to genetic diversity at local and regional scales. By combining long-term temperate and tropical forest studies across entire tree communities, the investigators will be able to parameterize models that incorporate functional and genetic variation among species to test predictions about current and future changes in forests.

The project will be implemented through a series of capacity-building initiatives that will expand science and enhance collaboration between the US and China. The strengthening of the network will have long-term benefits for American and Chinese researchers examining the role of forests in a changing global environment. The investigators will engage approximately 200 students and early-career scientists over five years. An international scientific exchange program will enable 10 US students and early-career researchers to spend 3 months in collaborating institutions in China. Chinese scientists will have similar opportunities in the US through a parallel proposal to NSF-China. These scientists will be drawn from the US, China, and other developing countries in Asia and the Americas. In addition, the scientific workshops will result in the development of new analytical tools and data compilations that will be made openly available through the web.

Recent news:

<http://news.harvard.edu/gazette/story/2011/07/gauging-forest-changes/>



Stuart Davies



Robert Howe

Above left: 25-ha deciduous forest plot at Changbaishan National Nature Reserve, China

Above right: 25-ha deciduous forest plot at Wabikon Lake Forest in Chequamegon Nicolet National Forest, USA



James Lutz

Left: 25-ha mixed conifer forest plot at Yosemite National Park, USA



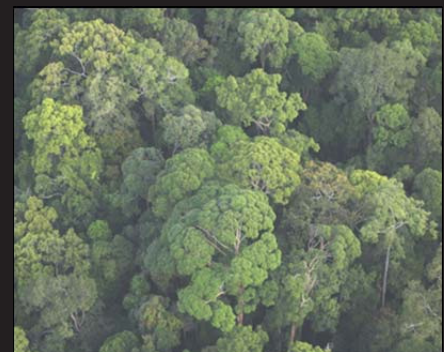
S. Davies

Right: Epiphytic growth in 50-ha plot at Yasuni National Park, Ecuador



Sabrina Russo

Left: Understory of the 52-ha lowland dipterocarp forest plot at Lambir Hills National Park, Malaysia



Christian Ziegler

Right: Canopy of the plot at Lambir Hills National Park, Malaysia

Below left: Seeds and fruits from the 50-ha plot at Huai Kha Khaeng Wildlife Sanctuary, Thailand

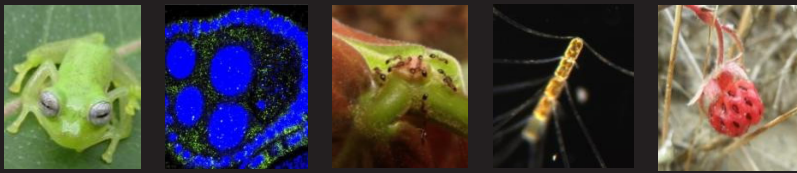
Below right: Researchers from the Center for Tropical Forest Science and the Chinese Forest Biodiversity Monitoring Network



C. Ziegler



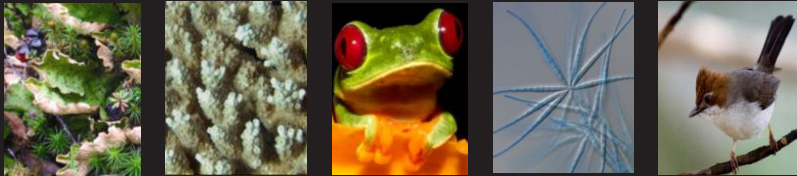
S. Davies



Row 1 (left to right):

1. Poff, NL (FY10): *Nymphargus wileyi*, a holotype of a new Ecuadorian species of centrolenid (glass frogs)
2. Douglas, AE (FY12): Micrograph of *Wolbachia* (green) associated with the egg chamber of a *Drosophila neotestacea*
3. Kursar, T (FY11): Ants at nectaries on expanding leaves of a Brazilian species of *Inga*
4. Stahl, DA (FY10): *Chaetoceros convolutus*, a marine planktonic diatom
5. Ashman, TL (FY12): *Fragaria chiloensis* fruit at Honeyman State Park, Florence, Oregon

Dimensions of Biodiversity



Row 2:

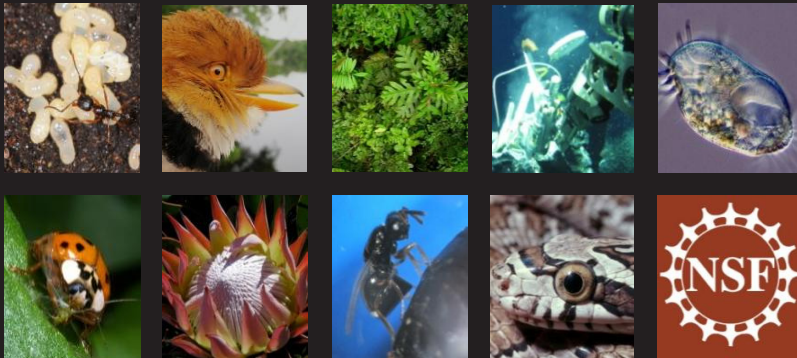
1. Moyle, LC (FY11): Tobacco hornworm (*Manduca sexta*) on an Andean wild tomato, *Solanum habrochaetes*
2. Moran, NA (FY10): Sonoran bumblebee, *Bombus sonorus*, on an hibiscus flower



National Science Foundation 2010 - 2012 Projects

Row 3:

1. Lutzoni, FM (FY10): Lichens (*Peltigera leucophlebia*) in close association with plants in a boreal forest
2. Rohwer, F (FY10): Close-up of coral polyps, *Acropora* sp
3. Belden, LK (FY11): A Panamanian red-eyed treefrog, *Agalychnis callidryas*
4. Ferrer, A (FY12): The mitosporic fungi, *Flabelliospora multiradiata* with conidia adapted to aquatic habitats
5. Martin, TE (FY12): *Yuhina*, an endemic species in Borneo with a wide elevational distribution



Row 4:

1. Gillespie, RG (FY12): A Hawaiian happy face spider, *Theridion grallator*, from the wet forest of Puu Kukui, West Maui
2. Dawson, MN (FY12): Endemic jellyfish *Mastigias papua etpisoni* in Ongeim'l Tketau, also called 'Jellyfish Lake'.

Row 5:

1. Sanders, NJ (FY11): A foraging ant of the *Aphaenogaster rudis* complex tending a brood of larvae and pupae
2. Bates, J (FY12): The collared puffbird, *Bucco capensis*, sallies for insects from hidden perches in the forest
3. Davies, SJ (FY10): Understory of a 52-ha lowland dipterocarp forest plot at Lambir Hills National Park, Malaysia
4. Sievert, SM (FY11): The submersible *Alvin* measures temperature, pH, and sulfide at "Crab Spa," a diffuse-flow hydrothermal vent site on the East Pacific Rise
5. Clamp, J (FY11): *Diophrys* sp., a hypotrich ciliate, one of the largest groups in the phylum Ciliophora

Row 6:

1. Ives, AR (FY12): The multicolored Asian ladybeetle, *Harmonia axyridis*.
2. Schlichting, CD (FY10): The king protea, *Protea cyanaroides*, national flower of South Africa
3. Bordenstein, S (FY10): A *Nasonia* parasitoid wasp using her ovipositor to deposit eggs inside a fly pupae
4. Brooks, T (FY11): *Pantherophis emoryi*, Great Plains ratsnake (Colorado, USA)